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09/818943 Eriksson et al. 3/28/01

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1) interference search

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Searcher Prep/Rev. Time: _____
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:08:39 ; Search time 118.5 Seconds
(without alignments)
1126.011 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSRLGLLVTSALAQRRGT.....DVALEHHBCDCVCRGSTGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	3	AAY84557 Amino aci
2	1858	100.0	345	5	AAB13212 Human pla
3	1858	100.0	345	8	ADR31425 Human pla
4	1851	99.6	345	2	AAY41766 Human PRO
5	1851	99.6	345	2	AAY30023 Human vas
6	1851	99.6	345	2	AAY33679 Human VEG
7	1851	99.6	345	3	AAB33414 Human PRO
8	1851	99.6	345	3	AAB19578 Human PRO
9	1851	99.6	345	3	AAB10651 Human VEG
10	1851	99.6	345	3	AAB10633 Human RAC
11	1851	99.6	345	3	AAB10650 Human 990
12	1851	99.6	345	3	AAB10635 Human VEG
13	1851	99.6	345	3	AAB10644 Human VEG
14	1851	99.6	345	3	AAB44322 Human PRO
15	1851	99.6	345	3	AAB24412 Human PRO
16	1851	99.6	345	3	AAY59285 Bone morp
17	1851	99.6	345	3	AAY96858 Human gro
18	1851	99.6	345	3	AAB48657 Human zve
19	1851	99.6	345	3	AAB01419 Human TAN
20	1851	99.6	345	3	AAB24250 Human pla
21	1851	99.6	345	3	AAB02649 Human LP8
22	1851	99.6	345	4	AAY12314 Human PRO
23	1851	99.6	345	4	AAB53074 Human ang
24	1851	99.6	345	4	AAB74028 Human VEG
25	1851	99.6	345	4	AAG65603 Human zve

ALIGNMENTS

RESULT 1

AY84557	AY84557	standard; protein, 345 AA.
XX	AY84557	
AC	AY84557	
XX	25-JUL-2000	(first entry)
DT	25-JUL-2000	
XX	Amino acid sequence of platelet-derived growth factor C (PDGF-C).	
DE	Amino acid sequence of platelet-derived growth factor C (PDGF-C).	
XX	Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.	
KW	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200018212-A2.	
FN	WO200018212-A2.	
XX	06-APR-2000.	
PD	06-APR-2000.	
XX	30-SEP-1999;	99WO-US022668.
PF	30-SEP-1999;	98US-0102461P.
XX	30-SEP-1998;	98US-0102461P.
PR	12-NOV-1998;	98US-0108109P.
PR	03-DEC-1998;	98US-0110749P.
PR	18-DEC-1998;	98US-0113002P.
PR	21-MAY-1999;	99US-0135426P.
PR	15-JUL-1999;	99US-0144022P.
XX	(LUDW-) LUDWIG INST CANCER RES.	
PA	(UYHE-) UNIV HELSINKI LICENSING LTD.	
PA	Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;	
FI	Oestman A, Heldin C, Betscholtz C;	
XX	WPI; 2000-292954/25.	
DR	N-PSDB; AAA12523.	
XX	Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C receptor.	
PT	Claim 27; Fig 2; 135pp; English.	
XX	The present sequence represents human platelet-derived growth factor C (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the	

CC ability to stimulate and enhance proliferation or differentiation, and/or
 CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C
 CC polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor and
 CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used
 CC for stimulating connective tissue or wound healing. The PDGF-C
 CC polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of PDGF-
 CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling
 CC during invasion of tumour cells into a normal population of cells.
 CC Antagonists can also be used to treat fibrotic conditions, especially
 CC found in the lung, kidney or liver
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 3; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6.2e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPVLPESA 180
 DB 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPVLPESA 180
 QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 QY 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345

RESULT 2
 AAE13212
 ID AAE13212 standard; protein; 345 AA.
 XX AAE13212;
 AC AAE13212;
 DT 12-FEB-2002 (first entry)
 XX Human platelet-derived growth factor (PDGF-C) protein.
 DE Human; transgenic animal; platelet derived growth factor C; PDGF-C;
 KW cardiac hypertrophy; fibrosis.
 KW Homo sapiens.
 OS WO200172132-A1.
 PN 04-OCT-2001.
 PD 28-MAR-2001; 2001WO-US009855.
 XX 28-MAR-2000; 2000US-0192507P.
 PR
 XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Eriksson U, Li X, Ponten A, Aase K, Li H;
 XX WPI; 2002-010700/01.
 DR A transgenic animal over-expressing platelet derived growth factor C is
 PT useful to study and find therapy for disease associated with PDGF-C over-
 PT expression, including cardiac hypertrophy and fibrosis.
 XX Disclosure; Page 40-42; 48pp; English.
 XX The patent discloses a method for producing a transgenic, non-human
 CC animal over-expressing a platelet derived growth factor C (PDGF-C), or
 CC its functional fragment or analogue. The method involves introducing a
 CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
 CC cell into a non-human animal and allowing the cell to develop into a
 CC transgenic, non-human animal. The transgenic animal is useful as a model
 CC to study disease states characterised by over-expression of PDGF-C and to
 CC find therapy for those diseases, particularly hypertrophy and fibrosis in
 CC various organs including the heart. The present sequence is PDGF-C
 CC protein from human
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 5; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6.2e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPVLPESA 180
 DB 121 GRWCGSGTVPGKQISKGNIQIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPVLPESA 180
 QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
 QY 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345

RESULT 3
 ADR31425
 ID ADR31425 standard; protein; 345 AA.
 XX ADR31425;
 AC ADR31425;
 DT 04-NOV-2004 (first entry)
 XX Human platelet derived growth factor C (PDGF-C) protein.
 DE VEGF; vascular endothelial growth factor; PDGF;
 KW platelet derived growth factor; gene therapy; myelosuppression;
 KW ischaemia; human.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT 23. .159
 FT /note = CUB domain of PDGF-C

FT	Domain	164..345	
FT	FT	/note = Minimal domain	
XX	PN	WO2004070018-A2.	
XX	XX	19-AUG-2004.	
XX	XX	04-FEB-2004; 2004WO-US03316.	
XX	PF	04-FEB-2003; 2003US-0445021P.	
XX	PR	16-MAY-2003; 2003US-0471412P.	
XX	XX	(LUDW-) LUDWIG INST CANCER RES.	
PA	PA	(LICN) LICENTIA LTD.	
XX	XX	(UYFL-) FLANDERS INTERUNIVERSITY INST BIOTECHNOL.	
PI	PI	Alitalo K, Eriksson U, Carmeliet P, Li X, Collen D;	
PI	PI	Yla-Herttuala S, Salven P, Rajantie R;	
XX	XX	WPI; 2004-604438/58.	
DR	DR	N-PSDB; ADR31424.	
XX	XX	Stimulating stem cell recruitment, proliferation, or differentiation to	
PT	PT	stimulate myelopoiesis by vascular endothelial growth factor B or	
FT	FT	platelet derived growth factor therapy.	
XX	XX	Claim 51; SEQ ID NO 7; 151pp; English.	
PS	PS	The present invention relates to a method of stimulating stem cell	
XX	XX	recruitment, proliferation, or differentiation to stimulate myelopoiesis	
CC	CC	by vascular endothelial growth factor B (VEGF-B) product or platelet	
CC	CC	derived growth factor (PDGF) therapy. The invention is useful in gene	
CC	CC	therapy and for treating myeloapression and ischaemia. The invention is	
CC	CC	also useful for manufacturing a medicament for mobilizing endothelial	
CC	CC	progenitor cells to the peripheral blood in a mammalian subject. The	
CC	CC	present sequence is human platelet derived growth factor C (PDGF-C)	
CC	CC	protein. This sequence is used to illustrate the method of invention.	
XX	XX	Sequence 345 AA;	
SQ	SQ	Query Match 100.0%; Score 1858; DB 8; Length 345;	
		Best Local Similarity 100.0%; Fred. No. 6.2e-179;	
		Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MSLFGLLVTSALAGQRGTQAESNLSSKFQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60	
Db	1	MSLFGLLVTSALAGQRGTQAESNLSSKFQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60	
QY	61	PRPPTYPRNTVLRVLAVERNVMWQLTDFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120	
Db	61	PRPPTYPRNTVLRVLAVERNVMWQLTDFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120	
QY	121	GRWCSSGTVPGQISKGQIRIRFVSDYDFPSEPGFCIHYNIMVQFTFTEAVSPSVLPESA 180	
Db	121	GRWCSSGTVPGQISKGQIRIRFVSDYDFPSEPGFCIHYNIMVQFTFTEAVSPSVLPESA 180	
QY	181	LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRVRVVDLNL 240	
Db	181	LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRVRVVDLNL 240	
QY	241	LTEEVRLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300	
Db	241	LTEEVRLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300	
QY	301	VTKKYHEVLQLPKPTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345	
Db	301	VTKKYHEVLQLPKPTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345	
RESULT 4			
AY41766			
ID	AY41766	standard; protein; 345 AA.	
XX	XX		

AC	AY41766;	
XX	XX	07-DEC-1999 (first entry)
XX	XX	Human PRO200 protein sequence.
DE	DE	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX	XX	probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW	KW	secreted protein; transmembrane protein.
XX	XX	Homo sapiens.
OS	OS	WO9946281-A2.
XX	XX	16-SEP-1999.
XX	XX	08-MAR-1999; 99WO-US005028.
XX	XX	10-MAR-1998; 98US-0077450P.
PR	PR	11-MAR-1998; 98US-0077632P.
PR	PR	11-MAR-1998; 98US-0077641P.
PR	PR	11-MAR-1998; 98US-0077649P.
PR	PR	12-MAR-1998; 98US-0077791P.
PR	PR	13-MAR-1998; 98US-0078004P.
PR	PR	17-MAR-1998; 98US-00040220.
PR	PR	20-MAR-1998; 98US-0078886P.
PR	PR	20-MAR-1998; 98US-0078910P.
PR	PR	20-MAR-1998; 98US-0078936P.
PR	PR	20-MAR-1998; 98US-0078939P.
PR	PR	25-MAR-1998; 98US-0079294P.
PR	PR	26-MAR-1998; 98US-0079656P.
PR	PR	27-MAR-1998; 98US-0079663P.
PR	PR	27-MAR-1998; 98US-0079664P.
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PR	PR	29-APR-1998; 98US-0083554P.
PR	PR	29-APR-1998; 98US-0083558P.

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PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 07-MAY-1998; 98US-0084627P.
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PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
- PA
XX (GETH ) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
DR N-PSDB; AAZ34296.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX Claim 12; Fig 207; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AAZ33891 to AAZ34338, and AA41685 to
XX AA41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENVMVQLTFDPRFGLDEPDICKYDFVEEPEPDSGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENVMVQLTFDPRFGLDEPDICKYDFVEEPEPDSGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSLPPSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSLPPSA 180
QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLKGAFVFGKRSRVDLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLKGAFVFGKRSRVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300
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QY 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHHEECDCVCRGSTGG 345
RESULT 5
AAAY30023
ID AAAY30023 standard; protein; 345 AA.
XX
AC AAAY30023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
XX Vascular endothelial growth factor related protein; VEGF-R protein;
XX tissue growth inhibition; tumour growth; cancer; tissue growth;
XX angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
PN WO9937671-A1.
XX
PD 29-JUL-1999.
XX
XX 26-JAN-1999; 99WO-US001574.
XX
XX 27-JAN-1998; 98US-0072635P.
PR 05-JUN-1998; 98US-0088089P.
PR 24-JUN-1998; 98US-0090544P.
PR 31-AUG-1998; 98US-0098548P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
XX Dou S, Na S, Song HY;
XX
XX WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
XX polynucleotide, useful for identifying antagonists and binding compounds.
XX
XX Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
XX related (VEGF-R) protein. VEGF-R can be used in assays to identify
XX compounds that bind to it or that antagonize its activity. VEGF-R
XX antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
XX tissue growth. This is useful for inhibiting tumour growth and for
XX treating cancer. VEGF-R itself can be used to stimulate tissue growth,
XX angiogenesis and to treat coronary artery blockage. The VEGF-R coding
XX sequence can be used for the recombinant production of the VEGF-R protein
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENVMVQLTFDPRFGLDEPDICKYDFVEEPEPDSGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENVMVQLTFDPRFGLDEPDICKYDFVEEPEPDSGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSLPPSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSLPPSA 180

```

QY 61 PRPHTYPRNTLVWRLVAEENWVWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 |||||
 DB 61 PRPHTYPRNTLVWRLVAEENWVWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 |||||
 QY 121 GRWCSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 |||||
 DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 |||||
 QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240
 |||||
 DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240
 |||||
 QY 241 LEEVRLYSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 |||||
 DB 241 LEEVRLYSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 |||||
 QY 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345
 |||||
 DB 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345
 |||||

RESULT 6
 ID AAY33679 standard; protein; 345 AA.
 XX
 AC AAY33679;
 XX
 DT 11-JAN-2000 (first entry)
 XX
 DE Human VEGF-E protein.
 XX
 KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO947677-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US005190.
 XX
 PR 17-MAR-1998; 98US-0040220.
 PR 02-NOV-1998; 98US-00184216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ferrara N, Kuo SS;
 XX
 DR WPI; 1999-580306/49.
 DR N-PSDB; AA223691.
 XX
 PT New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy.
 XX
 PS Claim 1; Fig 2; 122pp; English.
 XX
 CC This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy It
 CC can be combined with a carrier in pharmaceutical compositions, which can
 CC be administered to treat disorders as above. VEGF-E can be used to screen
 CC for antagonists and agonists, and the antagonists administered to treat
 CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-
 CC related macular degeneration. It can be used to generate antibodies,

CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-
 CC E can be used to diagnose cardiovascular and endothelial disorders in
 CC mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 2; Length 345;
 Best Local Similarity 99.4%; Pred. No. 3.1e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGQRGTQAESNLSSKFQFSSNKEQGVQDPOHERIITVSTNGSIHS 60
 |||||:|||||
 DB 1 MSLFGLLLVTSALAGQRGTQAESNLSSKFQFSSNKEQGVQDPOHERIITVSTNGSIHS 60
 |||||:|||||
 QY 61 PRPHTYPRNTLVWRLVAEENWVWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 |||||
 DB 61 PRPHTYPRNTLVWRLVAEENWVWQLTDFRFGLEDPEDDICKYDFVEEPEPSDGTIL 120
 |||||
 QY 121 GRWCSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 |||||
 DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 |||||
 QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240
 |||||
 DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240
 |||||
 QY 241 LEEVRLYSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 |||||
 DB 241 LEEVRLYSCTPRNFSVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 |||||
 QY 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345
 |||||
 DB 301 VTKKYHEVLQRLPKTGVRLHKSITDVALEHHEBCDCVCRGSTGG 345
 |||||
 RESULT 7
 ID AAB33414 standard; protein; 345 AA.
 XX
 AC AAB33414;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO200 protein UNQ174 SEQ ID NO:2.
 XX
 KW Human; immune related disease; diagnosis; antinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neutropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunologic disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.

XX WO200053758-A2.
PD 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005841.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0131445P.
XX 04-MAY-1999; 99US-0132371P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WL, Yan M;
XX
XX WPI; 2000-572271/53.
XX N-PSDB; AAC58579.
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 2; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel

CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
XX Sequence 345 AA;
SQ
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSNKGQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSNKGQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNTVLVWRLVAVEENVWIOITDERFGLDEPDIDICKYDFVEEPESDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVEENVWIOITDERFGLDEPDIDICKYDFVEEPESDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSEPFQFCIHYNVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSEPFQFCIHYNVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLPERWQDLEDLYRPTWOLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLPERWQDLEDLYRPTWOLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELARTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELARTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
QY 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
RESULT 8
AAB19578
ID AAB19578 standard; protein; 345 AA.
XX
XX AAB19578;
XX
XX 22-JAN-2001 (first entry)
XX
XX Human PRO200 (vascular endothelial growth factor E).
XX
XX PRO200; vascular epithelial growth factor E; VEGF-E; human;
KW ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;
KW macular degeneration; retinal detachment; retinal tear; macular hole;
KW myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;
KW contusion; edema; retinal vision occlusion; vascular disease;
KW retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1. .14
FT /label= Signal_peptide
FT Protein 15. .345
FT /label= Mature_Pro200
FT Modified-site 15. .21
FT /note= "N-myristoylation"
FT Modified-site 25. .29
FT /note= "Asn is N-glycosylated"
FT Modified-site 55. .59
FT /note= "Asn is N-glycosylated"
FT Modified-site 117. .123
FT /note= "N-myristoylation"
FT Modified-site 127. .133

FT Modified-site /note= "N-myristoylation"
 FT 254..258
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 281..287
 FT Modified-site /note= "N-myristoylation"
 FT 282..288
 FT Modified-site /note= "N-myristoylation"
 FT 319..325
 FT /note= "Amidation"
 XX
 PN WO200053760-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006319.
 XX
 PR 12-MAR-1999; 99US-0123957P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ;
 PI Kabakoff RC, Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WT;
 XX
 DR WPI: 2000-587437/55.
 DR N-PSDB; AAA88515.
 XX
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
 XX
 XX Claim 2; Fig 2; 140pp; English.
 PS
 CC The present sequence is that of human PRO200 or vascular endothelial
 CC growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515)
 CC that was isolated from a glioma cell line G61 library using probes (see
 CC AAA88523-26) based on an expressed sequence tag (see AAA88522) that
 CC showed homology to VEGF. PRO200 has a predicted mol. wt. of 39,029 and a
 CC pI of about 6.06. A method for producing PRO polypeptides, including
 CC PRO200, using a host cell transformed with a vector comprising a PRO
 CC nucleic acid is claimed. The invention relates to the use of PRO
 CC polypeptides to delay, prevent or rescue retinal cells such as retinal
 CC neurons selected from photoreceptors, retinal ganglion cells, displaced
 CC retinal ganglion cells, amacrine cells, displaced amacrine cells,
 CC horizontal and bipolar neurons, and supportive cells (including Mueller
 CC cells and pigment epithelial cells) from injury and degradation. The
 CC retinal cells are preferably photoreceptors and photoreceptor cell injury
 CC or death is caused by retinal injury, light or environmental trauma or by
 CC an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal tears,
 CC retinopathy, retinal degenerative diseases, macular holes, degenerative
 CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or
 CC contusion such as Purtscher's retinopathy, edema, ischemic conditions
 CC such as central or branch retinal vision occlusion, collagen vascular
 CC diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
 CC occlusion associated with Siles disease and systemic lupus erythematosus
 CC (claimed)
 XX
 SQ Sequence 345 AA;
 Query Match 99.6%; Score 1851; DB 3; Length 345;
 Best Local Similarity 99.4%; Pred. No. 3.1e-178;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQSSNKEONGVQDPOHERIITVSTNGSIHS 60
 DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKFQSSNKEONGVQDPOHERIITVSTNGSIHS 60
 QY 61 PRFPHYPRNTVLVRLVAEENWVLIQTDFERFGLDEPDIDCKYDFVEEPEFSDGTIL 120
 DB 61 PRFPHYPRNTVLVRLVAEENWVLIQTDFERFGLDEPDIDCKYDFVEEPEFSDGTIL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPSEPGFCIHYNVMPQTEAVSPVLPESA 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPSEPGFCIHYNVMPQTEAVSPVLPESA 180
 QY 181 LPLDLLANNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPLDLLANNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
 QY 241 LTERVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 DB 241 LTERVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
 QY 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
 RESULT 9
 AAB10651
 ID AAB10651 standard; protein; 345 AA.
 XX
 AC AAB10651;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Human VEGF-X protein #3.
 XX
 VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.
 XX
 OS Homo sapiens.
 XX
 WO2000037641-A2.
 XX
 29-JUN-2000.
 XX
 21-DEC-1999; 99WO-US030503.
 XX
 22-DEC-1998; 98GB-00028377.
 PR 18-MAR-1999; 99US-0124967P.
 PR 08-NOV-1999; 99US-0164131P.
 XX
 (JANC) JANSSEN PHARM NV.
 XX
 Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;
 Dhanaraj SN, Xu J;
 WPI; 2000-442669/38.
 XX
 New vascular endothelial growth factor protein, useful for treating or
 preventing diseases associated with inappropriate angiogenesis activity
 such as cancer, rheumatoid arthritis, psoriasis and wounds.
 XX
 Claim 72; Fig 12; 127pp; English.
 XX
 This invention describes a novel vascular endothelial growth factor-X
 (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 antidiabetic activity and acts as an angiogenesis and vascularization
 regulator. An antisense molecule of the invention is useful for treating
 or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 retinopathy by inhibiting angiogenic activity or inappropriate
 vascularization including formation and proliferation of new blood
 vessels, growth and development of tissues, tissue regeneration and organ
 and tissue repair in a subject. The products of the invention are useful
 for preparing medicaments for treating wounds such as dermal ulcers,
 pressure sores, venous sores, diabetic ulcers and burns and to promote
 skin graft growth, tissue repair, proliferation of new blood vessels,
 tissue regeneration and organ repair by promoting angiogenic activity or
 vascularization. This sequence represents the human VEGF-X protein
 described in the method of the invention

```
XX SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNTVLVRLVAEENVWIQLTDFRFGLEDPEDDICKYDFVEEPESDGTIL 120
DB 61 PRFPHYPRNTVLVRLVAEENVWIQLTDFRFGLEDPEDDICKYDFVEEPESDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLKAFFGGRKSRVVDLNL 240
DB 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLKAFFGGRKSRVVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCVRGSGTG 345
DB 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCVRGSGTG 345
RESULT 10
ID AAB10633
AC AAB10633;
XX
XX DT 19-JAN-2001 (first entry)
XX DE Human RACE generated VEGF-X protein.
XX
XX KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX OS Homo sapiens.
XX
XX PN WO200037641-A2.
XX PD 29-JUN-2000.
XX
XX PF 21-DEC-1999; 99WO-US030503.
XX
XX PR 22-DEC-1998; 98GB-00028377.
XX PR 18-MAR-1999; 99US-0124967P.
XX PR 08-NOV-1999; 99US-0164131P.
XX
XX PA (JANC ) JANSSEN PHARM NV.
XX
XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
XX PI Dhanaraj SN, Xu J;
XX
XX DR WPI: 2000-442669/38.
XX DR N-PSDB; AAA71951.
XX
XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
```

```
PS Disclosure; Fig 6; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNTVLVRLVAEENVWIQLTDFRFGLEDPEDDICKYDFVEEPESDGTIL 120
DB 61 PRFPHYPRNTVLVRLVAEENVWIQLTDFRFGLEDPEDDICKYDFVEEPESDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLKAFFGGRKSRVVDLNL 240
DB 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLKAFFGGRKSRVVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCVRGSGTG 345
DB 301 VTKKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCVRGSGTG 345
RESULT 11
AAB10650
ID AAB10650 standard; protein; 345 AA.
XX
XX AC AAB10650;
XX
XX DT 19-JAN-2001 (first entry)
XX
XX DE Human 990126veg protein.
XX
XX KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX OS Homo sapiens.
XX
XX PN WO200037641-A2.
XX
XX PD 29-JUN-2000.
```

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PF 21-DEC-1999; 99WO-US030503.
XX
XX 22-DEC-1998; 98GB-00028377.
PR 18-MAR-1999; 99US-0124967P.
PR 08-NOV-1999; 99US-0164131P.
XX
XX (JANC ) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX WPI; 2000-442669/38.
DR
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
XX Disclosure; Fig 11; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990136vegX protein
CC used to illustrate the method of the invention
XX
XX Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFLGILLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSFLGILLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLRVAVAEENVVNIQLTFDERFGLDEPDIDCKYDFVEVEEPSDGTIL 120
DB 61 PRFPHTYPRNTVLRVAVAEENVVNIQLTFDERFGLDEPDIDCKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTFEVRVLYSCTPRNSVSIRELKTDTIFWPGCLLVKRCGNACCLHNCNCCVPSK 300
DB 241 LTFEVRVLYSCTPRNSVSIRELKTDTIFWPGCLLVKRCGNACCLHNCNCCVPSK 300
QY 301 VTKKTHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKTHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
RESULT 12
AAB10635
ID AAB10635 standard; protein; 345 AA.
XX
AC AAB10635;
XX
```

```
DT 19-JAN-2001 (first entry)
XX Human VEGF-X protein #1 isolated from clones 4 and 7.
XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.
XX Homo sapiens.
XX WO200037641-A2.
XX 29-JUN-2000.
XX 21-DEC-1999; 99WO-US030503.
XX 22-DEC-1998; 98GB-00028377.
PR 18-MAR-1999; 99US-0124967P.
PR 08-NOV-1999; 99US-0164131P.
XX (JANC ) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX WPI; 2000-442669/38.
DR N-FSDB; AAA71955.
XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
XX Disclosure; Fig 9; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention
XX
XX Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFLGILLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSFLGILLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLRVAVAEENVVNIQLTFDERFGLDEPDIDCKYDFVEVEEPSDGTIL 120
DB 61 PRFPHTYPRNTVLRVAVAEENVVNIQLTFDERFGLDEPDIDCKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQFTAVSPSVLPSPA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
```

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 13
AAB10644
ID AAB10644 standard; protein; 345 AA.

XX AAB10644;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #4.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US030503.

XX 22-DEC-1998; 98GB-00028377.

XX 18-MAR-1999; 99US-0124967P.

XX 08-NOV-1999; 99US-0164131P.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;

XX Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX N-PSDB; AAA71990.

XX New vascular endothelial growth factor protein, useful for treating or

XX preventing diseases associated with inappropriate angiogenesis activity

XX such as cancer, rheumatoid arthritis, psoriasis and wounds.

XX Disclosure; Fig 30B; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents a human VEGF-X protein
XX described in the method of the invention

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 3.1e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSFLGLLLVTSALAGQRGTQAESNLSSKFOFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSFLGLLLVTSALAGQRGTQAESNLSSKFOFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRFPHTYPRNTVLVRLVAVEENVMIQLTDFERFGLDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAVEENVMIQLTDFERFGLDPEDDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFPSEBGFCHYHNVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPCKQISKGNQIRIRFVSDEYFPSEBGFCHYHNVMPQFTEAVSPVLPPSA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPSPK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 14

AAB44322
ID AAB44322 standard; protein; 345 AA.

XX AAB44322;

XX 08-FEB-2001 (first entry)

XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.

XX Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US004341.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 29-MAR-1999; 99US-0126773P.

XX 21-APR-1999; 99US-0130232P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 23-JUN-1999; 99US-0141037P.

XX 26-JUL-1999; 99US-0145698P.

XX 29-OCT-1999; 99WO-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028551.

XX 16-DEC-1999; 99WO-US030095.

XX 30-DEC-1999; 99WO-US031243.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI: 2000-611443/58.
 DR N-PSDB; AAC78582.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.

XX Claim 12; Fig 207; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytotatic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 3.1e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

DB 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFERFGLDEPDDICKYDFVEEPPSDGTIL 120

DB 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFERFGLDEPDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQTEAVSPVLPSSA 180

DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQTEAVSPVLPSSA 180

QY 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVDNL 240

DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKSRVDNL 240

QY 241 LTEEVRVLYSCTPRNFSVIRELKRDTIFWPGLLVKRCGNCACCLHNCNECQVPSK 300

DB 241 LTEEVRVLYSCTPRNFSVIRELKRDTIFWPGLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQRPKTVGRGLHKSLLTDVALEHHEECDCVCRGSTG 345

DB 301 VTKKYHEVLQRPKTVGRGLHKSLLTDVALEHHEECDCVCRGSTG 345

RESULT 15

ID AAB24412 standard; protein; 345 AA.

XX AAB24412;

XX 07-NOV-2000 (first entry)

XX Human PRO13 protein sequence SEQ ID NO:137.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 KW cytotatic; gene therapy; vaccine.
 XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;

PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;

PI Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2000-412154/35.

XX N-PSDB; AAA77621.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing

XX disorders in mammals.

XX Claim 72; Fig 50; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides

XX useful for preventing, diagnosing and treating disorders in mammals by

XX cardiovascular, endothelial or angiogenic disorder in mammals by

XX modulating cell proliferation, angiogenesis and cardiovascularisation,

XX and for identifying agonists and antagonists of these processes. The

XX nucleic acids and the proteins they encode may be used in the prevention,

XX treatment and diagnosis of diseases associated with inappropriate PRO

XX expression such as cardiovascular, endothelial or angiogenic disorders in

XX mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For

XX example, the nucleic acids (NCs) and vectors containing them and the PRO

XX polypeptide may be used to treat disorders associated with decreased PRO

XX expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent

XX nucleotide and protein sequences used in the exemplification of the

XX present invention

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 3.1e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

DB 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFERFGLDEPDDICKYDFVEEPPSDGTIL 120

DB 61 PRPHTYPRNTVLVRLVAIVENWVQLTDFERFGLDEPDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQTEAVSPVLPSSA 180

DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDEYFSEPGFCIHYNVMPQTEAVSPVLPSSA 180

Qy	181	LPLDLNNAITAFSTLEDLI	RYLEPERWQDLED	LYRPTWQLLGKAFV	GRKSRVVDNL	240
Db	181	LPLDLNNAITAFSTLEDLI	RYLEPERWQDLED	LYRPTWQLLGKAFV	GRKSRVVDNL	240
Qy	241	LTEEVRLYSCTPRNFSV	SIREELKRTDTI	FWPGCLLVKRCGNCAC	CLHNCNECQVPSK	300
Db	241	LTEEVRLYSCTPRNFSV	SIREELKRTDTI	FWPGCLLVKRCGNCAC	CLHNCNECQVPSK	300
Qy	301	VTKKYHEVLQLRPKTG	VGRGLHKS LTD	VALEHHEECDCVCRG	STGG	345
Db	301	VTKKYHEVLQLRPKTG	VGRGLHKS LTD	VALEHHEECDCVCRG	STGG	345

Search completed: September 3, 2005, 19:25:47
Job time : 122.5 secs

J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by two genes in the mouse genome.
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TAK>
A:Cross-references: GB:L35279; NID:9619860; PIDN:AAA41710.1; PID:9619861
C:Genetics:
A:Gene: GDB:BMPI; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I.
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; EGF homology; beta-hydroxyasparagine; bone; calcium; duplication; gl
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:132-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:91-142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 3.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
QY 55 NGSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQITFDERFGLDEPDDICKYDFVEVEE 113
DB 599 NGSITSPGMPKPEYPPKNCINQVLVAPTQYRISLQDFETEG-----NDVCKYDFVEVRS 653
QY 114 --PSDGTILRGWCGSGTVPKGQISKGNQIRIRFVSDYFPSPGFCIH 160
DB 654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGPKAHP 700
RESULT 11
I49540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I49540; MUID:94229342; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:9439606; PIDN:AAA37306.1; PID:9439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:718,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted
Query Match 9.1%; Score 169; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 3.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 55 NGSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQITFDERFGLDEPDDICKYDFVEVEE 113
DB 604 NGSITSPGMPKPEYPPKNCINQVLVAPTQYRISLQDFETEG-----NDVCKYDFVEVRS 658
QY 114 --PSDGTILRGWCGSGTVPKGQISKGNQIRIRFVSDYFPSPGFCIH 160
DB 659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGPKAHP 705
RESULT 12
A5362
procollagen I C-proteinase enhancer protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 15-Mar-2004
C:Accession: A5362
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show
J. Biol. Chem. 269, 26280-26285, 1994
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p
A:Reference number: A5362; MUID:95014462; PMID:7523404
A:Accession: A5362
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TAK>
A:Cross-references: GB:L33799; NID:9642907; PIDN:AAA61949.1; PID:9642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Keywords: extracellular protein; glycoprotein; pyroglyutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: C1r/C1s repeat homology <C1R1>
F:159-270/Domain: C1r/C1s repeat homology <C1R2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,431/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 8.3%; Score 154; DB 2; Length 449;
Best Local Similarity 33.8%; Pred. No. 2.6e-05;
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;
QY 56 GSIHSPRPHTYPRNTVLVWRLVA-VEENVMIQITFDERFGLDEPDDICKYDFVEV--- 111
DB 168 GLTTPNWPESDYPGIGSCSWHIIAPPDQV-IALTFF-EKFDLE--PDTYCRYDSVSFENG 223
QY 112 EEPDGTILRGWCGSGTVPKGQISKGNQIRIRFVSDYFPSPGFCIHVNIMVQPT--- 168
DB 224 AVSDSRRLGKFCGD-AVPGSISSEGNELLYQFVSDLSVTAD-GFSASYK-TLPRGTAK 280
QY 169 -----EAVSPSV-LPPSALP 182
DB 281 QGGPKRGTEPKVKLPKPSQP 302
RESULT 13
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanog
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: UNIPROT:P25723; GB:M76976; NID:9157305; PIDN:AAA28491.1; PID:9157306
C:Genetics:
A:Gene: FlyBase:tlid
A:Cross-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s re

C;Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1r1>
F:468-578/Domain: C1r/C1s repeat homology <C1r2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <C1r3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <C1r4>
F:900-1013/Domain: C1r/C1s repeat homology <C1r5>
F:1221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.0%; Score 148.5; DB 1; Length 1057;
Best Local Similarity 38.0%; Pred. No. 0.00022;
Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;
QY 50 ITVSTNGSIHSPRPHPTYPNTLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFV 109
DB 472 LKLTQDSIDSPNYPMDYKPCVWRITA-PDNHVALKF-QSPELE--KHDGCAYDFV 527
QY 110 EVEE--PSDGTILGRWCGSGTVPGKQISGNQIRIRFVSD 147
DB 528 EIRNGNHSRLIGRFCDGLKLPNIK-TRSNQMYIRFVSD 566

RESULT 14
A:Sequence: A59271
RA-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Rifael, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates complement
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:O00187; GB:Y09926; NID:G4007626; PIDN:CAA71059.1; PID:G40076
A:Experimental source: tissue liver
A:Note: submitted to GenBank, December 1996
A:Note: parts of this sequence, including the amino end of the mature protein, were determined
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: lp36.2-lp36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homology
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine protease
F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1r1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1r2>
F:300-361/Domain: complement factor H repeat homology <EH1>
F:366-430/Domain: complement factor H repeat homology <EH2>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 7.7%; Score 143.5; DB 1; Length 686;
Best Local Similarity 32.1%; Pred. No. 0.00035;
Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;
QY 55 NGSIHSPRPHPTYPNTLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEP 114
DB 193 SGELSSPEYPRYPKLSCTYS-ISLEEGFSVILDFVESFDVETHELCPYDFLKIQ-- 249
QY 115 SDGTTILGRWCGSGTVPGKQISGNQIRIRFVSDYPPSPFGCIHY 160

Db 250 TDBEHGPFCKG-TLPHRIETKSNVTITFTVTDE-SGDHTGWKIHY 293

RESULT 15

T31069
tolloid-BMP-1 like protein 1 - California sea hare
N:Alternate names: probable metalloprotease TBL-1
C:Species: Aplysia californica (California sea hare)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31069
R:Li, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, J.H.; Byrne, J.H.; Es-
J. Neurosci. 17, 755-764, 1997
A:Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatment
A:Reference number: Z20965; MUID:98007484; PMID:8987797
A:Accession: T31069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1070 <LIU>
A:Cross-references: UNIPROT:P91972; EMBL:U57369; NID:G1899041; PID:G1899042; PIDN:AA474
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat

Query Match 7.5%; Score 139.5; DB 2; Length 1070;
Best Local Similarity 21.9%; Pred. No. 0.0013;
Matches 70; Conservative 36; Mismatches 102; Indels 111; Gaps 17;
QY 56 GSIHSPRPHPTYPNTLVWRLVAEENWVQL--TFDERFGLDEPDDICKYDFVEVE 112
DB 529 GFLNSPAYDPYGDGVCEW-VIVREGYQVAFETAFETEF---DPD---CAYDYVEIR 581
QY 113 --EPDGTILGRWCGSGTVPGKQISGNQIRIRFVSDYPPSPFGCIHY----- 160
DB 592 DGDTKDSPLVGTCGTRT-PANAISTSRHLVVKVSDSM-QKGGFSASYLEEVDCEGE 639
QY 161 -----NIVMPQFTEAVSPSV 175
DB 640 DHGCHVCVNTLGSVECTCKIGYELHSDGKCEKACGGYLDAPSGTISSPSF-----PD 694
QY 176 LPPSALPLDLNNAITAPS-----TLEDLIRYLPERWQLDLDLYRPTWLLGKAFVFG 230
DB 695 YPPD-----KNCVWHISAPKGHITLVNFTMDLE-WRGDECEL-----DFVRVTNVVG 741
QY 231 RKSRRVVDLNLTEEVRLYSCTPRNFSVS--IREELKRTDTTFWPGCLL-----VKRCG 283
DB 742 NKER-----LGGQYCGFMAPPSTISLSNELRIEPRSDTLQKTGFSMDYADVDE 795
QY 284 CACLLHNCN-----ECQC 296
DB 796 NGGCKHICENTVGSFHCSC 814

Search completed: September 3, 2005, 19:30:37
Job time : 27.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:09:34 ; Search time 114.5 Seconds
(without alignments)
1542.946 Million cell updates/sec

Title: US-09-818-943-1
Perfect score: 1858
Sequence: 1 MSLFGLLLVTSALAGRRGT.....DVALEHHBECDCVCRGSTG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	2 Q9NRA1	Q9nra1 homo sapien
2	1851	99.6	345	2 Q9UL22	Q9ul22 homo sapien
3	1664	89.6	345	2 Q9QY71	Q9qy71 m fallotein
4	1662	89.5	345	2 Q8CI19	Q8ci19 mus musculus
5	1646	88.6	345	2 Q9QXK6	Q9eqx6 rattus norv
6	1635	88.0	345	2 Q9JHV8	Q9jnv8 mus musculus
7	1614	86.9	345	2 Q91946	Q91946 gallus gall
8	1260	67.8	258	2 Q8K429	Q8k429 rattus norv
9	741.5	39.9	370	2 Q9GZP0	Q9gzp0 homo sapien
10	740.5	39.9	364	2 Q9BWV5	Q9bwv5 homo sapien
11	737.5	39.7	370	2 Q925I7	Q925i7 mus musculus
12	736	39.6	370	2 Q9EQT1	Q9eqt1 rattus norv
13	669.5	36.0	300	2 Q6V9H4	Q6v9h4 myctolagus
14	435.5	23.4	261	2 Q8K2L3	Q8k2l3 mus musculus
15	190.5	10.3	923	1 NR1P_BRARE	Q8qfx6 brachydanio
16	190.5	10.3	923	2 Q69D88	Q69db8 brachydanio
17	183	9.8	3494	2 Q71C53	Q71c53 homo sapien
18	183	9.8	3623	2 Q60494	Q60494 homo sapien
19	182	9.8	691	2 Q57658	Q57658 gallus gall
20	181.5	9.8	871	2 Q6T869	Q6t869 brachydanio
21	181.5	9.8	959	2 Q69DB7	Q69db7 brachydanio
22	181.5	9.8	959	2 Q6RT22	Q6rt22 brachydanio
23	181.5	9.8	959	2 Q6T870	Q6t870 brachydanio
24	180	9.7	34	2 Q9JUM4	Q9jlm4 mus musculus
25	179.5	9.7	928	1 NR1P_XENLA	P28824 xenopus lae
26	176	9.5	707	1 BNP1_XENLA	P98070 xenopus lae
27	176	9.5	977	2 Q91925	Q91925 xenopus lae
28	176	9.5	3623	2 Q70244	Q70244 rattus norv
29	173.5	9.3	616	1 SPAN_STRPU	P98068 strongyloce
30	172	9.3	1012	2 Q9WVM6	Q9wvm6 mus musculus
31	171	9.2	735	2 Q57381	Q57381 xenopus lae

32 171 9.2 735 2 Q66KI3 Q66ki3 xenopus lae
33 171 9.2 1015 2 Q9Y6L7 Q9y6l7 homo sapien
34 171 9.2 1078 2 Q9UQ00 Q9uq00 homo sapien
35 169 9.1 241 2 Q92I35 Q92i35 rattus norv
36 169 9.1 775 2 Q6P550 Q6p550 mus musculus
37 169 9.1 986 1 BNP1_HUMAN P13497 homo sapien
38 169 9.1 991 1 BNP1_MOUSE P98063 mus musculus
39 169 9.1 991 2 Q6NZM2 Q6nzm2 mus musculus
40 165.5 8.9 145 2 Q8BP20 Q8bp20 mus musculus
41 165.5 8.9 926 2 Q8QZV7 Q8qzv7 mus musculus
42 164.5 8.9 555 2 Q9H2E2 Q9h2e2 homo sapien
43 164.5 8.9 901 2 Q9H2D5 Q9h2d5 homo sapien
44 164.5 8.9 901 2 Q9H2E4 Q9h2e4 homo sapien
45 164.5 8.9 906 2 Q9H2D4 Q9h2d4 homo sapien

ALIGNMENTS

RESULT 1
Q9NRA1
ID Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
RT receptor";
RL Nat. Cell Biol. 2:302-309(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSSP; Q9JJS8; INT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 2; Length 345;
Best Local Similarity 100.0%; Pred.No. 3.1e-150;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFPSSNKEQNGVQDPQHERIIIVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGRRGTQAESNLSSKFPSSNKEQNGVQDPQHERIIIVSTNGSIHS 60
Qy 61 PRFPHYTNTLVNRLVAEENVIQLTDFERFGLDEPDIDCKYDFVEVEPSDGTIL 120
Db 61 PRFPHYTNTLVNRLVAEENVIQLTDFERFGLDEPDIDCKYDFVEVEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFFPSEFGFCHYINVMQFTEAVSPSLPPSA 180

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Db 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSVLPSPA 180
QY 181 LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
Db 181 LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTGVRGLHSLTDVALEHHEEDCDVCRGSTGG 345
Db 301 VTKKYHEVLQLRPKTGVRGLHSLTDVALEHHEEDCDVCRGSTGG 345

RESULT 2
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Secretory growth factor-like protein fallotin (Spinal cord-derived growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name=hSCDGF; Synonyms=PDGFC; ORFNames=UN0174;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.-J., Lee R.K., Lin S.-P., Chen Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene, fallotin, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
RN FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.B., Humes J.M., Palmer T.E., Hart C.B.;
RA "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha and beta receptor.";
RN J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brush J., Eaton J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Ratten D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RN Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.

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DR EMBL; AF260738; AAK51637.1; -.
DR EMBL; AY358493; AAQ88857.1; -.
DR HSP; Q9JUS8; INTO.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 99.6%; Score 1851; DB 2; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.2e-149;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLVTSALAGORRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHITYPRNTVLVRLVAEENVMWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHITYPRNTVLVRLVAEENVMWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSVLPSPA 180
Db 121 GRWCSGTVPKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQTEAVSPSVLPSPA 180
QY 181 LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
Db 181 LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKGAFVFGKRSRVVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTGVRGLHSLTDVALEHHEEDCDVCRGSTGG 345
Db 301 VTKKYHEVLQLRPKTGVRGLHSLTDVALEHHEEDCDVCRGSTGG 345

RESULT 3
Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Fallotin (Platelet-derived growth factor C) (Mus musculus adult male cecum CDNA, RIKEN full-length enriched library, clone:9130403008 product:platelet-derived growth factor, C polypeptide, full insert DE sequence) (Mus musculus 7 days neonate cerebellum CDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15 days embryo head CDNA, RIKEN full-length enriched library, DE clone:B930001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence).
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RN Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,

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RA Gilbertson D., West J., O'Hara P.J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RX MEDLINE=21085860; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RA The FANTOM Consortium;
 RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RL "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RL "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 DR EMBL: AF117608; AAF22516.1; -;
 DR EMBL: AF266467; AKS58566.1; -;
 DR EMBL: AK033734; BAC28455.1; -;
 DR EMBL: AK042767; BAC31358.1; -;
 DR EMBL: AK052947; BAC35216.1; -;
 DR HSP: Q9JUS8; 1NT0.
 DR MGD: MGI:1859631; Pdgc.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0005161; F:platelet-derived growth factor receptor bin.; IDA.
 DR GO: GO:0008284; P:positive regulation of cell proliferation; IDA.

DR GO: GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla.; IDA.
 DR GO: GO:0007171; P:transmembrane receptor protein tyrosine kin.; IDA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00341; PDGF; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS02278; PDGF 2; 1.
 KW Growth factor; Mitogen.
 SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
 Query Match 89.6%; Score 1664; DB 2; Length 345;
 Best Local Similarity 86.7%; Pred. No. 1.2e-133;
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MSLFGLLVTSALAGQRRGTOAESNLSSKFFSNKQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MLLGLGLLVTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPHERVVTISNGSIHS 60
 QY 61 PRPHTYPRNTLVRLVAVEENWVQLTDFERGLEDPEDDICKYDFVEEESDGTIL 120
 DB 61 PKFHTYPRNVLVRLVAVDENVRIQLTDFERGLEDPEDDICKYDFVEEESDGSVL 120
 QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDIEYFPSEFGFCIHYNVMPQFTEAVSPVLPPSA 180
 DB 121 GRWCGSGTVPKGQISKGNHIRFVSDIEYFPSEFGFCIHYSIIMPQVTTTSPVLPPSS 180
 QY 181 LPDLLNNAITAFSTLEDLIRYLPERWQDLEDLYRPTWOLGKAFVFGKRSRVVDLNL 240
 DB 181 LSLDLLNNAITAFSTLEELIRYLPEDRWQDLDLYRPTWOLGKAFYGGKSKVYNLNL 240
 QY 241 LTBVRLVSYCTPRNFVSIRRELKRTDTIFWPGCLLVKRCGNCACCLHNCQCQVPSK 300
 DB 241 LKEVKLYSYCTPRNFVSIRRELKRTDTIFWPGCLLVKRCGNCACCLHNCQCQVPRK 300
 QY 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
 DB 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
 RESULT 4
 Q8C119
 ID Q8C119 PRELIMINARY; PRT; 345 AA.
 AC Q8C119
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Platelet-derived growth factor, C polypeptide.
 GN Name=PDGf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2ECB II; TISSUE=Mammary tumor;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; 1NT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
KW SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;
SQ
Query Match 89.5%; Score 1662; DB 2; Length 345;
Best Local Similarity 86.4%; Pred. No. 1.7e-133;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;
QY .
Db 1 MSLFGLLVTALAGORRGTOAESNLSSKQFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60
1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVTVISNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENVMQITFDRFGLDEPDIDCKYDFVEEPEPSDGTIL 120
61 PKFHTYPRNTVLVRLVAEENVMQITFDRFGLDEPDIDCKYDFVEEPEPSDGTIL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPSEPGFCIHYNVMPQTEAVSPVLPPSA 180
121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
181 LSLLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSKVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNAGG 345
DB
RESULT 5
Q3EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=rsdcgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JUS8; 1NT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
KW SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;
SQ
Query Match 89.5%; Score 1662; DB 2; Length 345;
Best Local Similarity 86.4%; Pred. No. 1.7e-133;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;
QY .
Db 1 MSLFGLLVTALAGORRGTOAESNLSSKQFQSSNKEQNGVQDPOHERIITVSTNGSIHS 60
1 MLLGLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPHRRVTVISNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENVMQITFDRFGLDEPDIDCKYDFVEEPEPSDGTIL 120
61 PKFHTYPRNTVLVRLVAEENVMQITFDRFGLDEPDIDCKYDFVEEPEPSDGTIL 120
QY 121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPSEPGFCIHYNVMPQTEAVSPVLPPSA 180
121 GRWCSGTVPGKQISKGNQIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPVLPPSS 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
181 LSLLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSKVVDLNL 240
QY 241 LTEEVRVLSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSTGG 345
301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGNAGG 345
DB
RESULT 6
Q3UHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
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DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

Query Match 67.8%; Score 1260; DB 2; Length 258;
Best Local Similarity 85.6%; Pred. No. 2.6e-99;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;

QY 42 QDPOHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVTQLTFDERFGLDEPED 101
Db 1 QDPRHVVVTISGNSIHSKPEPHTYPRNTVLVRLVAEENVTQLTFDERFGLDEPED 60

QY 102 DICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVDSDEYFPPSPGCIHYN 161
Db 61 DLCKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNHIRIRFVDSDEYFPPSPGCIHYS 120

QY 162 IVMPOFTVAVSPSVLPSPGALPDLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWQ 221
Db 121 IIMPQVTTTSVLPSPGALSJDLNNAVTAFTVEELIRFLEPRWQIDLSLYKPTWP 180

QY 222 LIGKAFVGRKRVVDLNLLEVEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 281
Db 181 LLGKAFLYGKSKAVNLLKEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 240

QY 282 GNCACCLHNCNECQVCP 298
Db 241 GNCACCLHNCNECQVCP 257

RESULT 9
Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth factor D) (iris-expressed growth factor long form).
GN Name=hSCGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCGF-B, a novel growth factor homologous to SCGF/PDGF-C/fallotainin";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S., Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J., Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liaw C.C., Zhao M.S., Hui R.T.;
RA Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chilla K.R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.B., Yang M., Vernet C., Burgess C.E., Fernandez E., Degler L.L., Rittman B., Shinkets J., Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Uutela M., Li X., Pietras K., Ostman A., Heidin C.H., Alitalo K., Eriksson U.;

"PDGF-D is a specific, protease-activated ligand for the PDGF beta-receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berse D., Smith D., Peterson K.;
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank project: steroid-response factors and similarities with retinal pigment epithelium";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; --
DR EMBL; AF113216; AAG39287.1; --
DR EMBL; AF335584; AAK38840.1; --
DR EMBL; AF336376; AAK56136.1; --
DR EMBL; AY027517; AAK20081.1; --
DR PIR; JC7591; JC7591.
DR HSP; Q9JUS8; IN70.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674_CRC64;

Query Match 39.9%; Score 741.5; DB 2; Length 370;
Best Local Similarity 43.6%; Pred. No. 8.1e-55;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 3 LFGLLVTSALAGQRGTQAESNLSSKQFSSN---KEQNGVQD-POHERIITVSTNGSI 58
Db 5 IFVYTLICANFCSCRDTSATPSASIKALRNANLRDESNHLLTDLRYRDETIOVKGNGYV 64

QY 59 HSPFPHTYPRNTVLVRLVAEENVTQLTFDRFGLDEPEDDICKYDFVEVEPSDGT 118
Db 65 QSPFPNSYPRNLLTWRLHS-QENTRIQLVDFDQFGLAEANDICRTDFVEVEIDSETS 123

QY 119 --ILGRWCGSGTVPGKQISKGNQIRIRFVDSDEYFPPSPGCIHYNVMPQFTEAV----- 171
Db 124 TIIRGRCGHEVPPRIKSRNQIKITFKSDDYFVAKGPKIYYSYL-LEDQPAASSETN 182

QY 172 -----SPSVLPSPGALPDLNNAITAFSTLEDLIRYLEPERWOLDLEDLYR 217
Db 183 WESVTSSTSGSVNSPSTDP-T-LIADALDKKIAEFDTVEDLLKYFPNSEQEDLENNYL 241

QY 218 PTWOLLGKAFVGRKRVVDLNLLEVEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLV 277
Db 242 DTPYRGSY-HDRASK-VDLRLNDKAKYSCIPRYSVNIIRBELKLANVVFPRCLLV 299

QY 278 KRCGNCACCLHNCNECQVSPKTKYKHYEVLQRP---KTGVRGLHKSLLTDVALEHHEE 334
Db 300 QRCGNCGCGTVNWRSCNCSGKTKYKHYEVLQRPFGHIKRRGRAKTWALVDIQLDHHH 359

QY 335 CDCVC 339
Db 360 CDCIC 364

RESULT 10
Q9BWV5 PRELIMINARY; PRT; 364 AA.
AC Q9BWV5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)


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Db 220 VEDLLKYPASQWDDLENDLYMDTPRYGRSY-HERKSK-VLDRLNDVVKYSCTPRNH 277
QY 256 SVSIREELKRTDTITWPGCLLVKRCGNCACCLHNCNECQCVPKVTYKHYEVLQLRP-- 313
Db 278 SVNREELKLTNAVFPFRCCLLVQRCGNCAGCCTLWKSCTCSSGKTVKHYEVLKPEFQH 337
QY 314 -KTGVRGLHKSITDVALEHHESCDVC 339
Db 338 FRRRGKAKNMALVDIQLDHERCDCTC 364

RESULT 13
Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Irie-expressed growth factor (fragment).
GN Name=PDGFG;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
* FT NON_TER 1
* FT NON_TER 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 36.0%; Score 669.5; DB 2; Length 300;
Best Local Similarity 45.9%; Pred. No. 8.9e-49;
Matches 139; Conservative 51; Mismatches 86; Indels 27; Gaps 8;

QY 52 VSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQLTDFERFGLDEPDDICKYDFVEV 111
Db 2 VTGNHGVQSAPFNSYPRNLLTLWRLHS--QEKTRIQALAFDHQFGLAEADICRYDFVEV 60

QY 112 EEPSPDGT--ILGRWCGSGTVPKQISKGNQIRFVSDYEPSPGFCIHYNIV----- 163
Db 61 EDISTSTVIRGWCGHKEVPRITSRNQIKITFKSDDYFVAKGFKIYGFVEDFQPA 120

QY 164 -----MPQTEAVS-----PSVLPPSALPLDLNNAITAFSTLEDLIRYLEPERWQD 211
Db 121 AASNTWESVTSISGVSVHNSVTDPT-LTADALDKTIABPDTVEDLLKHFNPSQWQED 179

QY 212 LEDLYRPTWQLGKAFVGRKSRVVDLMLTVEVRLYCTPRNFVSIREELKRTDTTFW 271
Db 180 LENLYDTPHYGRSY-HDRKSK-VLDRLNDADAKRYSCTPRNVSNLEELKLTNVVFF 237

QY 272 PCCLLVKRCGNCACCLHNCNECQCVPKVTYKHYEVLQLRP---KTGVRGLHKSITDVA 328
Db 238 FRCCLLVQRCGNCAGCCTVNWKSCTCSSGKTVKHYEVLKPEFQHFRNRNKNMALVDIQ 297

QY 329 LEH 331
Db 298 LDH 300

RESULT 14

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Q8K2L3 PRELIMINARY; PRT; 261 AA.
ID Q8K2L3;
AC Q8K2L3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pdgid protein.
GN Name=PDGFG;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030896; AAH30896.1; -.
DR HSP; Q90JUS8; INT0.
DR MGD; MG1:1919035; Pdgid.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 23.4%; Score 435.5; DB 2; Length 261;
Best Local Similarity 33.8%; Pred. No. 7.3e-29;
Matches 97; Conservative 45; Mismatches 73; Indels 29; Gaps 7;

QY 16 QRRGTQAESNLSSKFQSSNKEQGVOD--PQHERIITVSTNGSIHSPRPHTYPRNTVLV 74
Db 26 QRASIKALRNANLR-----RDES NHLTDLYQRENIQVTSNGHVQSFRFPNSYPRNLLT 80

QY 75 WRLVAEENWVQLTDFERFGLDEPDDICKYDFVEEPEPSDGT--ILGRWCGSGTVPK 132
Db 81 WRLRS-QEKTRIQSLSDHFQFGLAEADICRYDFVEEVEESSTVVRGRCGKHKEIPPR 139

QY 133 QISKGNQIRFVSDYEPSPGFCIHYNIVMPQTEAV-----SPS 174
Db 140 ITSRTNQIKITFKSDDYFVAKPGFKIYYSFYFVDSQPEAASSETNWESVTSSFSVSYHSPS 199

QY 175 VLPPSALPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSR 234
Db 200 ITDPT-LTADALDKTVAEFDTEVLLKHFNPSQWQDLENDLYDTPHYGRKSY-HDRKSK 257

235 VVDL 238

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Db          258 GIEV 261
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RESULT 15
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ID NRPI BRARE STANDARD; PRT; 923 AA.
AC Q8QF6; Q8AXP1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neurophilin-1 precursor (znrlp).
GN Name=nrpl; Synonyms=up-1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
[1]_SEQUENCE FROM N.A., FUNCTION, AND DEVELOPMENTAL STAGE.
RP STRAIN=AB; TISSUE=Embryo;
RC PubMed=12142468; DOI=10.1073/pnas.162366299;
RA Lee P., Goishi K., Davidson A.J., Mannix R., Zon L., Klagsbrun M.;
RT "Neurophilin-1 is required for vascular development and is a mediator
of VEGF-dependent angiogenesis in zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10470-10475(2002).
RN [2]_SEQUENCE FROM N.A.
RA Shoji W., Tawarayama H.;
RT "The cloning and expression of neurophilin-1.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor involved in the development of the
cardiovascular system, in angiogenesis, in the formation of
certain neuronal circuits and in organogenesis outside the nervous
system. It mediates the chemorepulsant activity of semaphorins.
CC Regulates angiogenesis through a VEGF-dependent pathway.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
Maternal transcripts are widely expressed until the early gastrula
stage, then become localized to the yolk syncytial layer. During
somatogenesis and later stages of development, expression occurs
mainly in neuronal and vascular tissues.
CC -!- SIMILARITY: Belongs to the neurophilin family.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AY064213; RAL40862.1; -.
CC EMBL; AB088776; BAC53657.1; -.
CC HSSP; O14786; IKEX.
CC ZFIN; ZDB-GENE-030519-2; nrpl.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000421; FAS8 C.
CC InterPro; IPR008979; Gal_Bind_like.
CC InterPro; IPR000998; MAM.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FAS8C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FAS8C_1; 1.
CC PROSITE; PS01286; FAS8C_2; 2.
CC PROSITE; PS50022; FAS8C_3; 2.

DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS50060; MAM_2; 1.
KW Angiogenesis; Glycoprotein; Neurogenesis; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 923 Neurophilin-1.
FT DOMAIN 20 856 Extracellular (Potential).
FT TRANSMEM 857 877 Potential.
FT DOMAIN 878 923 Cytoplasmic (Potential).
FT DOMAIN 25 139 CUB 1.
FT DOMAIN 145 263 CUB 2.
FT DOMAIN 273 422 F5/8 type C 1.
FT DOMAIN 429 581 F5/8 type C 2.
FT DOMAIN 642 811 MAM.
FT DISULFID 25 52 Probable.
FT DISULFID 80 102 Probable.
FT DISULFID 145 171 Probable.
FT DISULFID 204 226 Probable.
FT DISULFID 273 422 By similarity.
FT DISULFID 429 581 By similarity.
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 520 520 N-linked (GlcNAc...) (Potential).
FT CONFLICT 230 230 T -> S (in Ref. 2).
FT CONFLICT 317 317 K -> E (in Ref. 2).
FT CONFLICT 454 454 T -> S (in Ref. 2).
FT CONFLICT 463 463 L -> M (in Ref. 2).
FT CONFLICT 617 617 G -> D (in Ref. 2).
SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.3%; Score 190.5; DB 1; Length 923;
Best Local Similarity 27.6%; Pred. No. 3e-07; Mismatches 29; Indels 49; Gaps 8;
Matches 66; Conservative 29;

QY 5 GLLLVTSALAGQRGCTQAESNLSSKFPQSSNKQNGVQDPQHERIITVSTNGSIHSRPP 64
DB 12 GFLIVSALKNDKCGDN-----IRTSANYLTSPGVP 43
QY 65 HTYPRNTVLVRLVAEENVMQLTFDERFGLDEDDICKYDFVEVEPSD--GTLGR 122
DB 44 VSYTPSQKCIWITAPGNQRIILNFNPHFLEDR---CKYDYVEVRDGVDENGQLVGK 100
QY 123 WCGSGTVPGKQISKGNQIRIRVSDYFPSPGFCIHYNIVMP-----QFTEAVSPSVL 176
DB 101 YCGK-IAPSPVSSGNQLFIKPVSD-YETHGAGSIRYEIPKGTGECRNFTS--SSGVI 156
QY 177 PPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWOLGKAFVFGKSRV 235
DB 157 KSPGPFKEYPNNDCTFMIFAPKMSIIVLEFESPELEPTQP-----PAGVFCRYDL 209

Search completed: September 3, 2005, 19:29:41
Job time : 117.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:19:05 ; Search time 30 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSFLGLLVTSALAGRRGT.....DVALEHHEECDCVCRGSTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*

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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appli
2	1851	99.6	345	US-09-457-086-2	Sequence 2, Appli
3	1851	99.6	345	US-09-265-686-2	Sequence 2, Appli
4	1851	99.6	345	US-09-540-224-5	Sequence 5, Appli
5	1851	99.6	345	US-09-564-595D-33	Sequence 33, Appli
6	1851	99.6	345	US-09-706-968-2	Sequence 2, Appli
7	1851	99.6	345	US-09-723-749-2	Sequence 2, Appli
8	1851	99.6	345	US-09-823-033-2	Sequence 2, Appli
9	1851	99.6	345	US-09-468-647A-101	Sequence 101, App
10	1851	99.6	345	US-09-468-647A-110	Sequence 110, App
11	1851	99.6	345	US-09-468-647A-130	Sequence 130, App
12	1851	99.6	345	US-10-139-583-2	Sequence 2, Appli
13	1851	99.6	374	US-09-468-647A-118	Sequence 118, App
14	1843	99.2	345	US-09-468-647A-2	Sequence 2, Appli
15	1843	99.2	345	US-09-468-647A-103	Sequence 103, App
16	1757	94.6	355	US-09-468-647A-122	Sequence 122, App
17	1755	94.5	354	US-09-468-647A-120	Sequence 120, App
18	1747	94.0	323	US-09-468-647A-1	Sequence 1, Appli
19	1664	89.6	345	US-09-457-066-43	Sequence 43, Appli
20	1664	89.6	345	US-09-564-595D-35	Sequence 35, Appli
21	1664	89.6	345	US-09-706-968-43	Sequence 43, Appli
22	1664	89.6	345	US-09-823-033-4	Sequence 4, Appli
23	1664	89.6	345	US-10-139-583-43	Sequence 43, Appli
24	1443	5	77.7	US-09-468-647A-112	Sequence 112, App
25	1325	71.3	302	US-09-564-595D-54	Sequence 54, Appli
26	1266.5	68.2	303	US-09-564-595D-57	Sequence 57, Appli
27	1098	59.1	316	US-09-564-595D-55	Sequence 55, Appli

Sequence 56, Appli
Sequence 111, App
Sequence 27, Appli
Sequence 126, App
Sequence 37, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 37, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 37, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 53, Appli
Sequence 4, Appli
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-040-220D-2

; Sequence 2, Application US/09040220D

; Patent No. 6391311

; GENERAL INFORMATION:

; APPLICANT: Kuo, Sophia S.

; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC

; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,

; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION

; FILE REFERENCE: P1122

; CURRENT APPLICATION NUMBER: US/09/040,220D

; CURRENT FILING DATE: 1998-03-17

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 2

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Human

; US-09-040-220D-2

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Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSFLGLLVTSALAGRRGTQAESNLSSKTFQSSNKQNGVQDPQHERIITVSTNGSIHS	60
Db	1	MSFLGLLVTSALAGRRGTQAESNLSSKTFQSSNKQNGVQDPQHERIITVSTNGSIHS	60
Qy	61	PRPHTYPRNTVLVWRLVAEENWVQLTDEREGLEDDEDDICKYDFVEVEEPSDGTIL	120
Db	61	PRPHTYPRNTVLVWRLVAEENWVQLTDEREGLEDDEDDICKYDFVEVEEPSDGTIL	120
Qy	121	GRWCGSTVFGKQISKGNQIRFVSDYFSEPGFCIHYNVMPQTEAVSPVLPSPA	180
Db	121	GRWCGSTVFGKQISKGNQIRFVSDYFSEPGFCIHYNVMPQTEAVSPVLPSPA	180
Qy	181	LPDLLNNAITAFSTLLEDLIRYLEPERWQDLEDLYPTWQLLGKAFVFGKRSRVVDLNL	240
Db	181	LPDLLNNAITAFSTLLEDLIRYLEPERWQDLEDLYPTWQLLGKAFVFGKRSRVVDLNL	240
Qy	241	LTEVRVLYSCTPRNFSVSIREELKRTDTIWPFGCLLVKRCGGNCACCLHNCNECQVPSK	300
Db	241	LTEVRVLYSCTPRNFSVSIREELKRTDTIWPFGCLLVKRCGGNCACCLHNCNECQVPSK	300
Qy	301	VTKKYHEVLQLRPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG	345
Db	301	VTKKYHEVLQLRPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG	345

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RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Chul O.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300

QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300

QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 3
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
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US-09-265-686-2

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300

QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGQRGTOAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPTYPRNTVLVRLVAEENWVWQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSEPGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVP SK 300

QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
```


QY 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345
Db 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345

RESULT 5

US-09-564-595D-33
; Sequence 33, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-564-595D-33

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPFSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPFSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
QY 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345
Db 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345

RESULT 6

US-09-706-968-2
; Sequence 2, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-706-968-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPFSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPFSEPGFCIHYNIVMPQTEAVSPVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSRVVDLNL 240
QY 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LEEVRLVSCPTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345
Db 301 VTKYHEVLQRPKTVGRLHKLSTDLVALEHHEECDCVCRGSTG 345

RESULT 7

US-09-723-749-2
; Sequence 2, Application US/09723749
; Patent No. 6620784
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2D1
; CURRENT APPLICATION NUMBER: US/09/723,749
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Human
US-09-723-749-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345
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RESULT 9
US-09-468-647A-101
; Sequence 101, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: DiJkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: BOL92.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-101

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVWRLVAEENVMWQLTDFRFGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPGKQISKGNOIRIRFVSDYFPESEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 10
US-09-468-647A-110
; Sequence 110, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: DiJkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
```

; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-110

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 11
US-09-468-647A-130
; Sequence 130, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 345

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-130
Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 12
US-10-139-583-2
; Sequence 2, Application US/10139583
; Patent No. 6814965
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-2

Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.3e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLDEPDIDCKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPVLPESA 180

Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Qy 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 13
US-09-468-647A-118
; Sequence 118, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.7001IUS00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-118

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RESULT 14
US-09-468-647A-2
; Sequence 2, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.7001IUS00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-2
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Best Local Similarity 99.1%; Pred. No. 6.2e-192;
Matches 342; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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US-09-468-647A-103
; Sequence 103, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X

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; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-103

Query Match      99.2%; Score 1843; DB 4; Length 345;
Best Local Similarity 99.1%; Pred.No. 6.2e-192;
Matches 342; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      121 GRWCGSGTVPGKQISKGNIQIRFVSDYFSEPGFCIHYNIIVMPQFTEAVSPSVLPESA 180
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Qy      181 LPDLNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKRSRVVDLNL 240
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Db      301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:21:57 ; Search time 109.5 Seconds
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1240.813 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSFLGLLVTSALAGRRGT.....DVALEHHECDVCVRGSTGG 345

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Total number of hits satisfying chosen parameters: 1774312

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1858	100.0	345	9	US-09-852-209A-3
3	1858	100.0	345	13	US-10-086-823-32
4	1858	100.0	345	14	US-10-260-539-32
5	1858	100.0	345	14	US-10-131-600-3
6	1858	100.0	345	15	US-10-303-997B-3
7	1858	100.0	345	15	US-10-439-337A-3
8	1858	100.0	345	15	US-10-772-927A-7
9	1851	99.6	345	9	US-09-823-033-2
10	1851	99.6	345	9	US-09-923-995-4
11	1851	99.6	345	9	US-09-795-006A-149

12	1851	99.6	345	9	US-09-978-395A-488	Sequence 488, App
13	1851	99.6	345	9	US-09-978-697-488	Sequence 488, App
14	1851	99.6	345	9	US-09-978-192A-488	Sequence 488, App
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16	1851	99.6	345	10	US-09-978-189-488	Sequence 488, App
17	1851	99.6	345	10	US-09-796-753-6	Sequence 6, Appli
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21	1851	99.6	345	10	US-09-978-403A-488	Sequence 488, App
22	1851	99.6	345	10	US-09-978-564A-488	Sequence 488, App
23	1851	99.6	345	10	US-09-999-833A-488	Sequence 488, App
24	1851	99.6	345	10	US-09-981-915A-488	Sequence 488, App
25	1851	99.6	345	10	US-09-978-824-488	Sequence 488, App
26	1851	99.6	345	10	US-09-918-585A-488	Sequence 488, App
27	1851	99.6	345	10	US-09-999-834A-488	Sequence 488, App
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29	1851	99.6	345	10	US-09-978-193A-488	Sequence 488, App
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40	1851	99.6	345	10	US-09-978-299A-488	Sequence 488, App
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43	1851	99.6	345	10	US-09-978-802A-488	Sequence 488, App
44	1851	99.6	345	11	US-09-876-813-33	Sequence 33, Appl
45	1851	99.6	345	11	US-09-999-831A-488	Sequence 488, App

ALIGNMENTS

RESULT 1

US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-818-943-1

Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSFLGLLVTSALAGRRGTQAESNLSSKFQSSKQNGVQDPQHERIITVSTNGSIHS 60

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RESULT 2

US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209A-3

Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

US-10-086-623-32
; Sequence 32, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32

Query Match 100.0%; Score 1858; DB 13; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32

Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDEICKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDEICKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSLPESA 180
Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSLPESA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240

Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
Qy 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHBECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHBECDCVCRGSTGG 345

RESULT 5

US-10-131-600-3
; Sequence 3, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3

Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDEICKYDFVEVEEESDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLDEPDDEICKYDFVEVEEESDGTIL 120
Qy 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSLPESA 180
Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSLPESA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPFSK 300

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QY 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345
|||||
DB 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 6
US-10-303-997B-3
; Sequence 3, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGENESIS
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 345
; ORGANISM: Homo sapiens
US-10-303-997B-3

Query Match 100.0%; Score 1858; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
|||||
DB 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPPTYPRNTVLVRLVAEENWVQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
|||||
DB 61 PRPPTYPRNTVLVRLVAEENWVQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTAVSPSVLPSPA 180
|||||
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTAVSPSVLPSPA 180

QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
|||||
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
|||||
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

QY 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345
|||||
DB 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 7
US-10-439-337A-3
; Sequence 3, Application US/10439337A
; Publication No. US20040053837A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGENESIS
; FILE REFERENCE: 029065.44740C4
; CURRENT APPLICATION NUMBER: US/10/439,337A
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/303,997
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 345
; ORGANISM: Homo sapiens
US-10-439-337A-3

Query Match 100.0%; Score 1858; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
|||||
DB 1 MSLFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPPTYPRNTVLVRLVAEENWVQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120
|||||
DB 61 PRPPTYPRNTVLVRLVAEENWVQLTDFERFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTAVSPSVLPSPA 180
|||||
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTAVSPSVLPSPA 180

QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
|||||
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240

QY 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
|||||
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

QY 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345
|||||
DB 301 VTKYHEVLQRLPKTGVRLHKSLLTDVALEHHEECDCVCRGSTGG 345
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; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,021
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/471,412
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-927A-7

Query Match      100.0%; Score 1851; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORCTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORCTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCRCGSTGG 345
DB 301 VTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCRCGSTGG 345

RESULT 10
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4

Query Match      99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGTQAESNLSSKFOFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORRGTQAESNLSSKFOFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
QY 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
DB 241 LEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
QY 301 VTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCRCGSTGG 345
DB 301 VTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEEDCVCRCGSTGG 345

RESULT 11
US-09-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al

Query Match      99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORCTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSLFGLLLVTSALAGORCTQAESNLSSKFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
DB 61 PRPHTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLFGLLLVTSALAGORGTQAESNLSSKFOFSSNKQGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORGTQAESNLSSKFOFSSNKQGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRFPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVRLVAVEENVWIQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPKGQISKGNQIRIRFVSDIEYFSPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDIEYFSPSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180
Qy 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
Qy 301 VTKKYHEVLQLRPKTGVRLHLSLTDVALEHHBECDCVCRGSTGG 345
Db 301 VTKKYHEVLQLRPKTGVRLHLSLTDVALEHHBECDCVCRGSTGG 345

RESULT 13
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/085697

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Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PRFPHTYPRNTVLVRLVAENVNVIQLTDFRFRGLEDPEDDICKYDFVEVEEPSDGTIL 120
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Db 61 PRFPHTYPRNTVLVRLVAENVNVIQLTDFRFRGLEDPEDDICKYDFVEVEEPSDGTIL 120
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QY 121 GRWCSGTVPGKQISKGNOIRIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPSVLPESA 180
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QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVDNLNL 240
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QY 241 LTEEVRVLSCTPRNFSVSIRESLKRDTTIFWPGCLLVKRCGNACCLHNCNECQVPSK 300
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RESULT 14

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US-09-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085697

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Db	121	GRWCGSGTVPGKQISKGNOIRIRFVSDBYFPSEPGFCIHYNIVMPOFTAEVSPSVLPESA	180
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Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-173;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2005, 19:08:39 ; Search time 118.5 Seconds
(without alignments)
1126.011 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
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2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1848	100.0	345	4 AAE00998	Aae00998 Mouse zve
5	1848	100.0	345	5 AEG92894	Aeg92894 Mouse VEG
6	1848	100.0	345	5 AAB13213	Aab13213 Mouse pla
7	1848	100.0	345	5 AAB47890	Aab47890 Mouse zve
8	1848	100.0	345	6 ABU72435	Abu72435 Mouse zve
9	1848	100.0	345	6 ABG76398	Abg76398 Mouse gro
10	1848	100.0	345	7 ADG47752	Adg47752 Mouse zve
11	1848	100.0	345	8 ADJ32788	Adj32788 Mouse zve
12	1848	100.0	345	8 ADL18359	Adl18359 Mouse zve
13	1667	90.2	345	2 AAY41766	Aay41766 Human PRO
14	1667	90.2	345	2 AAY30023	Aay30023 Human vas
15	1667	90.2	345	2 AAB33679	Aab33679 Human VEG
16	1667	90.2	345	3 AAB33414	Aab33414 Human PRO
17	1667	90.2	345	3 AAB19578	Aab19578 Human PRO
18	1667	90.2	345	3 AAB10651	Aab10651 Human VEG
19	1667	90.2	345	3 AAB10633	Aab10633 Human RAC
20	1667	90.2	345	3 AAB10650	Aab10650 Human 990
21	1667	90.2	345	3 AAB10635	Aab10635 Human VEG
22	1667	90.2	345	3 AAB10644	Aab10644 Human VEG
23	1667	90.2	345	3 AAB44322	Aab44322 Human PRO
24	1667	90.2	345	3 AAB24412	Aab24412 Human PRO
25	1667	90.2	345	3 AAY59285	Aay59285 Bone morph

26	1667	90.2	345	3 AAY96858	Aay96858 Human gro
27	1667	90.2	345	3 AAB48657	Aab48657 Human zve
28	1667	90.2	345	3 AAB01419	Aab01419 Human TAN
29	1667	90.2	345	3 AAB24250	Aab24250 Human pla
30	1667	90.2	345	4 AAE02649	Aae02649 Human Lp8
31	1667	90.2	345	4 AAU12314	Aau12314 Human PRO
32	1667	90.2	345	4 AAB53074	Aab53074 Human ang
33	1667	90.2	345	4 AAB74028	Aab74028 Human VEG
34	1667	90.2	345	4 AAG65603	Aag65603 Human zve
35	1667	90.2	345	4 AAU08465	Aau08465 Polypepti
36	1667	90.2	345	4 AAB50980	Aab50980 Human PRO
37	1667	90.2	345	4 AAB49895	Aab49895 Human PRO
38	1667	90.2	345	4 AAE00997	Aae00997 Human zve
39	1667	90.2	345	5 ABB79984	Abb79984 Human VEG
40	1667	90.2	345	5 ABG92889	Abg92889 Human VEG
41	1667	90.2	345	5 AAB47889	Aab47889 Human zve
42	1667	90.2	345	5 ABB81331	Abb81331 Human VEG
43	1667	90.2	345	5 AAU76684	Aau76684 Human zve
44	1667	90.2	345	6 ABO17758	Abol17758 Novel hum
45	1667	90.2	345	6 ABU72434	Abu72434 Human zve

ALIGNMENTS

RESULT 1

AAy84559
ID AAY84559 standard; protein; 345 AA.
XX
AC AAY84559;
XX
DT 25-JUL-2000 (first entry)
XX
DE A murine platelet-derived growth factor C (PDGF-C).
XX
KW Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling.
XX
OS Mus sp.
XX
PN WO200018212-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022668.
XX
PR 30-SEP-1998; 98US-0102461P.
PR 12-NOV-1998; 98US-0108109P.
PR 03-DEC-1998; 98US-0110749P.
PR 18-DEC-1998; 98US-0113002P.
PR 21-MAY-1999; 99US-0135426P.
PR 15-JUL-1999; 99US-0144022P.
XX
(LUDWIG-) LUDWIG INST CANCER RES.
(UYHE-) UNIV HELSINKI LICENSING LTD.
PA Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;
PI Oestman A, Heldin C, Betsholz C;
XX
DR N-PSDB; AAA12525.
XX
PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor.
XX
PS Claim 27; Fig 6; 135pp; English.
XX
CC The present sequence represents murine platelet-derived growth factor C
(PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the

CC ability to stimulate and enhance proliferation or differentiation, and/or
 CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C
 CC polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor and
 CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used
 CC for stimulating connective tissue or wound healing. The PDGF-C
 CC polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of PDGF-
 CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling
 CC during invasion of tumour cells into a normal population of cells.
 CC Antagonists can also be used to treat fibrotic conditions, especially
 CC found in the lung, kidney or liver
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSIHS 60
 DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSIHS 60

- QY 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEPSDGSVL 120
 DB 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPEPFCIHYSIIMQVTTTSPVLPSS 180
 DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPEPFCIHYSIIMQVTTTSPVLPSS 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVNNL 240
 DB 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300

QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCRGNAGG 345
 DB 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCRGNAGG 345

RESULT 2
 AAY96861
 ID AAY96861 standard; protein; 345 AA.
 XX
 AC AAY96861;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Murine vascular endothelial growth factor homologue, ZVEGF3.
 XX
 KW Vascular endothelial growth factor; homologue; zveg3; CUB domain;
 KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
 KW Chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;
 KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
 KW vulnery.
 XX
 OS Mus musculus.
 XX
 PN WO200034474-A2.
 XX
 PD 15-JUN-2000.
 XX
 XX 07-DEC-1999; 99WO-US028968.

XX 07-DEC-1998; 98US-00207120.
 PR 06-JUL-1999; 99US-0142578P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 PI WPI; 2000-423420/36.
 DR N-PSDB; AAA51527.
 XX
 PT Novel zveg3 polypeptides and nucleotides encoding them useful for
 PT stimulating growth of smooth muscle cells and fibroblasts comprising an
 PT epitope bearing portion of a specific amino acid sequence.
 XX
 PS Claim 1; Page 169-170; 173pp; English.

XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor
 CC homologue. Polypeptides comprising an epitope-bearing portion human or
 CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor
 CC domain and a CUB domain (generic sequence motifs are shown in AAY96859
 CC and AAY96860). The growth factor domain is characterized by an
 CC arrangement of cysteine residues and beta-strands that is characteristic
 CC of the "cysteine knot" structure of the platelet-derived growth factor
 CC (PDGF) family. The CUB domain shows homology to CUB domains in
 CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
 CC protein, bovine acidic seminal fluid protein and Xenopus laevis tollid-
 CC like protein. Structural analysis and homology predict that ZVEGF3
 CC polypeptides complex with a second polypeptide to form multimeric
 CC proteins. The human zveg3 gene has been mapped to chromosome 4q28.3.
 CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
 CC muscle cells, for activating cell surface PDGF-alpha receptor and for
 CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
 CC useful for regulating (post-development) organ growth, regeneration and
 CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
 CC antagonists are useful for treating cancer, rheumatoid arthritis, disease,
 CC diabetic retinopathy, ischemic limb disease, peripheral vascular disease,
 CC myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound
 CC healing, chronic liver disease and haemangioma formation. ZVEGF3 can also
 CC be used to modulate neurite growth and development of the nervous system,
 CC and for treating neurodegenerative diseases

Sequence 345 AA;
 Query Match 100.0%; Score 1848; DB 3; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSIHS 60
 DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISNGSIHS 60

QY 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEPSDGSVL 120
 DB 61 PKFPHYPRNMVWRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPEPFCIHYSIIMQVTTTSPVLPSS 180
 DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPEPFCIHYSIIMQVTTTSPVLPSS 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVNNL 240
 DB 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKVNNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300

QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCRGNAGG 345
 DB 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCRGNAGG 345

Db 301 VTKKYHEVLQRLPKTVGKGLHKSLLTDVALEHHEBCDCVCRNAGG 345

RESULT 3

AAB48658
ID AAB48658 standard; protein; 345 AA.

AC AAB48658;

DT 09-MAR-2001 (first entry)

DE Mouse zveg3, SEQ ID NO:35.

XX Mouse; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family;
KW murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic.

XX Mus musculus.

OS WO200066736-A1.

PN 09-NOV-2000.

PD 03-MAY-2000; 2000WO-US040047.

PR 03-MAY-1999; 99US-00304216.

PR 10-NOV-1999; 99US-0164463P.

PR 04-FEB-2000; 2000US-0180169P.

XX (ZYMO) ZYMOGENETICS INC.

PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.

DR N-PSDB; AAC81583.

XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.

XX Disclosure; Page 130-131; 143pp; English.

XX The invention relates to the human growth factor homologue zveg4
CC (AAB48653), and nucleic acids encoding it (AAC81585). Zveg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zveg4 or fragments thereof, particularly human zveg4/human zveg3
CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a method
CC of modulating the proliferation, differentiation, migration or metabolism
CC of bone cells, comprising exposing bone cells to zveg4-derived
CC polypeptides; and a method of detecting a genetic abnormality in the
CC zveg4 gene of a patient. Zveg4 proteins and derived fragments may be
CC used to stimulate tissue development or repair, or cellular
CC differentiation or proliferation. They are particularly used for the
CC treatment or repair of liver damage, and may also be used to modulate
CC neurite growth (e.g., in the treatment of Alzheimer's disease or multiple
CC sclerosis). Due to their osteogenic activity, they may be used in the
CC treatment of periodontal disease and fractures. They may also be used to
CC enhance expansion and mobilisation of haematopoietic stem cells and
CC endothelial precursor stem cells, which may be useful in the treatment of
CC ischaemia, in wound healing, and in the modulation of the immune system.
XX The present sequence represents mouse zveg3

XX
SQ

Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60

QY 61 PKPHTYPRNNVWLVAVDENVRILQTFDERFGLDEPDDICKYDFVEEPEPSDGSVL 120
DB 61 PKPHTYPRNNVWLVAVDENVRILQTFDERFGLDEPDDICKYDFVEEPEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDRYFFSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHIRFVSDRYFFSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LSLDLNNAVTAFTLELIRYLPDRMQVDLSLYKFTWQLLKAFYKSKVYNLNL 240
DB 181 LSLDLNNAVTAFTLELIRYLPDRMQVDLSLYKFTWQLLKAFYKSKVYNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCVPRK 300

QY 301 VTKKYHEVLQRLPKTVGKGLHKSLLTDVALEHHEBCDCVCRNAGG 345

DB 301 VTKKYHEVLQRLPKTVGKGLHKSLLTDVALEHHEBCDCVCRNAGG 345

RESULT 4

AAB00998

ID AAB00998 standard; protein; 345 AA.

XX AC AAB00998;

XX 04-JUL-2001 (first entry)

DE Mouse zveg3 protein.

XX Mouse; Zveg3 antagonist; cell proliferation; stellate cell activation;
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KW fibroproliferative disorder.

XX Mus musculus.

XX WO200128586-A1.

XX 26-APR-2001.

XX 23-OCT-2000; 2000WO-US029270.

XX 21-OCT-1999; 99US-0161653P.

XX 12-NOV-1999; 99US-0165255P.

XX 01-AUG-2000; 2000US-022223P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gilbertson DG;

XX WPI; 2001-300278/31.

XX N-PSDB; AAD04650.

PT Use of zvegf3 antagonist for reducing fibroproliferative disorder of
PT kidney, liver and bone, reducing extracellular matrix production,
PT treating fibrosis or reducing stellate cell activation in mammal.
XX Example 2; Fig 2; 70pp; English.

XX The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a zvegf3 antagonist in combination
CC with a delivery vehicle. The zvegf3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
CC -antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchitis obliterans, organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibroproliferative disorders of the
CC vasculature such as transplant vasculopathy and fibroproliferative
CC disorders of the bone such as osteopetrosis and hyperostosis. The present
CC sequence is mouse zvegf3 protein

XX Sequence 345 AA;

- Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTTGAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60
Db 1 MLLGLLLTSLAGORTTGAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60
QY 61 PKFPHYTPNNVLVRLVAVDENVRIQLTFDERFGLDEPDICKYDFVEEPEPDSGVL 120
Db 61 PKFPHYTPNNVLVRLVAVDENVRIQLTFDERFGLDEPDICKYDFVEEPEPDSGVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCGRNAGG 345
Db 301 VTKKHEVLQRPKTVGKGLHSLTDVALEHHEEDCDVCGRNAGG 345

RESULT 5
ABG92894
ID ABG92894 standard; protein; 345 AA.
XX AC ABG92894;
XX 19-NOV-2002 (first entry)
XX Mouse VEGF-like protein zvegf 3.
XX VEGF; vascular endothelial growth factor; zvegf 3; mouse; chromosome 3;
KW cell proliferation; differentiation; metabolism; migration;
KW revascularisation; solid tumour; diabetic retinopathy; psoriasis;
KW rheumatoid arthritis; cancer; autoimmune disease; inflammation;
KW myocardial ischaemia; scleroderma; fibrosis; glomerulosclerosis;

KW atherosclerosis; skin wound; ulcer; burn; skin grafting;
KW female reproductive tract disorder; chronic liver disease;
KW circulatory disorder; heart failure; neurodegenerative disease;
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
KW neurite outgrowth.
XX Mus musculus.
OS US6432673-B1.
XX 13-AUG-2002.
XX 07-DEC-1999; 99US-00457066.
XX 07-DEC-1998; 98US-0111773P.
PR 06-JUL-1999; 99US-0142576P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
XX (ZYMO) ZYMOGENETICS INC.
PA Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX WPI: 2002-689759/74.
DR N-PSDB; ABS68648.
XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
PT ulcers, burns, skin grafting, female reproductive tract disorders,
PT Parkinson's disease, and Alzheimer's disease.
XX Example 4; Fig 2; 68pp; English.

CC The invention relates to an isolated polypeptide, designated zvegf3 (a
CC vascular endothelial growth factor-like protein) of 111-136 amino acid
CC residues in length and comprises the sequence appearing as ABG92889 from
CC amino acid residues 235-345. Also included are an isolated protein
CC comprising a first polypeptide disulphide bonded to a second polypeptide,
CC where each of the first and second polypeptides is from zvegf 3, and
CC where the protein modulates cell proliferation, differentiation,
CC metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3
CC expression vectors and host cells. Zvegf 3 is useful as additives in
CC tissue adhesives for promoting revascularisation of the healing tissue,
CC for designing molecules that antagonise semaphorin-stimulated activities,
CC including neurite growth, cardiovascular development, cartilage and limb
CC development, and T and B-cell function, and for imaging tumours or other
CC sites of abnormal cell proliferation and in gene therapy applications.
CC The proteins are useful therapeutically to stimulate tissue development
CC or repair, or cellular differentiation or proliferation, for stimulating
CC the growth of fibroblast or smooth muscle cells, as molecular weight
CC standards, as reagents in assays for determining circulatory level of the
CC protein or as standards in the analysis of cell phenotype, for reducing
CC identifying inhibitors of their activity which are useful for reducing
CC the growth of solid tumours, for treating diabetic retinopathy,
CC psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune
CC disease, inflammation, myocardial ischaemia, scleroderma, and reducing
CC fibrosis, including scar formation, keloids, liver fibrosis, lung
CC fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including
CC diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,
CC ulcers, burns, skin grafting, and female reproductive tract disorders,
CC chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's
CC disease, circulatory disorders e.g. heart failure, hepatic or portal vein
CC thrombosis, cardiac sclerosis, neurodegenerative diseases such as
CC multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for
CC regenerating neurite outgrowths following strokes. The gene for mouse
CC zvegf3 is located on chromosome 3. The present sequence represents zvegf
CC 3

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKPHTYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLNL 240
DB 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345

RESULT 6
AAE13213
ID AAE13213 standard; protein; 345 AA.
XX AAE13213;
DT 12-FEB-2002 (first entry)
DE Mouse platelet-derived growth factor (PDGF-C) protein.
XX
KW Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;
KW cardiac hypertrophy; fibrosis.
OS Mus sp.
XX
PW WO200172132-A1.
XX
XX
PD 04-OCT-2001.
XX
XX
PF 28-MAR-2001; 2001WO-US009855.
XX
PR 28-MAR-2000; 2000US-0192507P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Eriksson U, Li X, Ponten A, Aase K, Li H;
XX WPI; 2002-010700/01.
DR
XX
XX A transgenic animal over-expressing platelet derived growth factor C is
PT useful to study and find therapy for disease associated with PDGF-C over-
PT expression, including cardiac hypertrophy and fibrosis.
XX
XX Example 4; Page 42-43; 48pp; English.
PS
XX The patent discloses a method for producing a transgenic, non-human
CC animal over-expressing a platelet derived growth factor C (PDGF-C), or
CC its functional fragment or analogue. The method involves introducing a
CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the
CC cell into a non-human animal and allowing the cell to develop into a
CC transgenic, non-human animal. The transgenic animal is useful as a model
CC to study disease states characterised by over-expression of PDGF-C and to
CC find therapy for those diseases, particularly hypertrophy and fibrosis in
CC various organs including the heart. The present sequence is PDGF-C
CC protein from mouse
XX
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKPHTYPRNMVLRVAVDENVRVQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLNL 240
DB 181 LSLLDNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
RESULT 7
AAB47890
ID AAB47890 standard; protein; 345 AA.
XX AAB47890;
AC AAB47890;
DT 16-MAY-2002 (first entry)
XX
DE Mouse zveg3.
XX
KW Human; mouse; zveg3; zveg4; platelet derived growth factor; PDGF;
KW homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;
KW chondrocyte; bony defect; fracture; bone graft; implant;
KW periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
XX
OS Mus musculus.
XX
XX US2002004225-A1.
XX
XX 10-JAN-2002.
XX
XX 29-MAR-2001; 2001US-00823033.
XX
XX 07-DEC-1998; 98US-0111173P.
PR 06-JUL-1999; 99US-0142576P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165255P.
PR 07-DEC-1999; 99US-00457066.
PR 31-MAR-2000; 2000US-0193723P.
XX
XX (HART/) HART C E.
PA (GILB/) GILBERTSON D G.
XX
XX Hart CE, Gilbertson DG;
XX
XX WPI; 2002-171026/22.
DR N-PSDB; AA172444.
XX
XX Promoting growth of bone, ligament or cartilage in a mammal, involves
PT administering to the mammal a protein which comprises growth factor
PT domain of zveg3 protein, a homolog of platelet-derived growth factor.
XX
XX Claim 1; Page 19-20; 31pp; English.

XX The sequences given in AAB47889-90 represent human and mouse zvegfg3,
 CC respectively. zvegfg3 is a platelet derived growth factor (PDGF) homolog
 CC and it was used in the method of the invention for promoting growth of
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
 CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
 CC protein of residues 235-345 of human zvegfg3 or all of the mouse zvegfg3
 CC protein, with a delivery vehicle. The method of th invention is useful
 CC for promoting growth of bone, ligament or cartilage in a mammal, where
 CC the composition is administered at a site of a bony defect, preferably a
 CC fracture, bone graft site, implant site, or periodontal pocket, and for
 CC stimulating proliferation of osteoblasts or chondrocytes in a mammal. It
 CC is further useful for promoting proliferation of osteoblasts.
 CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLIGLLLTSLAQORTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
 DB 1 MLLIGLLLTSLAQORTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
 QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFERFGLDEPDICKYDFVEEPEPSDGSVL 120
 DB 61 PKFPHYPRNMVLRVAVDENVRVQLTDFERFGLDEPDICKYDFVEEPEPSDGSVL 120
 QY 121 GRWCSGTPVGKQTSKGNHIRFVSDYFPEPFGFCIHYSIIMPQVTTTSPSLPSS 180
 DB 121 GRWCSGTPVGKQTSKGNHIRFVSDYFPEPFGFCIHYSIIMPQVTTTSPSLPSS 180
 QY 181 LSLDLLNNVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYLGKSKVVNNL 240
 DB 181 LSLDLLNNVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYLGKSKVVNNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345
 DB 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345

RESULT 8
 ABU72435
 ID ABU72435 standard; protein; 345 AA.

XX AC ABU72435;

XX DT 16-JUN-2003 (first entry)

XX DE Mouse ZVEGF4-related protein #1.

XX Growth factor homologue; ZVEGF4; proliferation; differentiation;
 KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
 KW neurite growth; cardiovascular development; limb development;
 KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
 KW autoimmune disease; inflammation; retinopathy; haemangioma;
 KW ischaemic event; neuropathy; acute nerve damage; stroke;
 KW central nervous system disease; peripheral nervous system disease.

XX Mus musculus.

XX US6495668-B1.

XX 17-DEC-2002.

XX 03-MAY-2000; 2000US-00564595.

XX 03-MAY-1999; 99US-0132250P.
 PR 10-NOV-1999; 99US-0164463P.
 PR 04-FEB-2000; 2000US-0180169P.
 XX (ZYMO) ZYMOGENETICS INC.
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 XX WPI; 2003-352153/33.
 DR N-PSDB; ACA64137.
 XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
 PT composition as, e.g. therapeutic agents, diagnostic agents, and research
 PT tools and reagents, includes polypeptides from amino acid residues.
 XX Disclosure; Col 95-98; 67pp; English.

XX The invention relates to an isolated protein comprising a first
 CC polypeptide disulphide-bonded to a second polypeptide. The first and
 CC second polypeptides are from 113-138 amino acid residues and comprises
 CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
 CC protein stimulates proliferation, differentiation, or migration of
 CC mesenchymal cells and may modulate activities mediated by cell surface
 CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
 CC semaphorin interactions which may be of use in neurite growth,
 CC cardiovascular development, cartilage and limb development, T- and B-cell
 CC functions as well as treating rheumatoid arthritis, various forms of
 CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
 CC ischaemic events, neuropathies, acute nerve damage, central nervous
 CC system diseases and peripheral nervous system diseases including stroke.
 CC The isolated protein is also used for a pharmaceutical composition as
 CC therapeutic agents, diagnostic agents, and research tools and reagents.
 CC It can be used in the study and regulation of cell and tissue
 CC development, as components of cell culture media. The proteins can form
 CC homodimers or heterodimers that act on tissues to control organ
 CC development by modulating cell proliferation, migration, differentiation,
 CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
 CC -23.1. A transgene construct was made for producing mice transgenic for
 CC human ZVEGF4. The construct contained human growth hormone gene control
 CC regions. The present sequence is a ZVEGF4-related protein sequence. Note:
 CC The present sequence is included in the sequence listing but is not
 CC mention elsewhere in the specification

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAQORTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
 DB 1 MLLIGLLLTSLAQORTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
 QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFERFGLDEPDICKYDFVEEPEPSDGSVL 120
 DB 61 PKFPHYPRNMVLRVAVDENVRVQLTDFERFGLDEPDICKYDFVEEPEPSDGSVL 120
 QY 121 GRWCSGTPVGKQTSKGNHIRFVSDYFPEPFGFCIHYSIIMPQVTTTSPSLPSS 180
 DB 121 GRWCSGTPVGKQTSKGNHIRFVSDYFPEPFGFCIHYSIIMPQVTTTSPSLPSS 180
 QY 181 LSLDLLNNVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYLGKSKVVNNL 240
 DB 181 LSLDLLNNVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYLGKSKVVNNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345
 DB 301 VTKKYHEVLQLRPKTGVKGLHSLTDVALEHHEECDCVCRNAGG 345

RESULT 9
 ABG76398
 ID ABG76398 standard; protein; 345 AA.
 AC ABG76398;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Mouse growth factor homologue, zvegfg3.
 XX
 KW Mouse; growth factor homologue; zvegfg3; fibroblast; smooth muscle cell;
 KW cell-surface platelet-derived growth factor alpha receptor; PDGF;
 KW full-thickness skin wound; female reproductive tract; duodenal ulcer;
 KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
 KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
 KW chronic active hepatitis; hepatic chronic passive congestion; stroke;
 KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;
 KW portal vein thrombosis; cardiac sclerosis; new vessel formation;
 KW endothelial precursor stem cell; neovascularisation; wound healing;
 KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
 KW sensory neurite outgrowth; brain damage; head injury; paralysis;
 KW spinal injury; neurodegenerative disease; diabetic retinopathy;
 KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
 KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
 KW proliferative vascular disorder; ocular neovascularisation;
 KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;
 KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;
 KW vulnerary; tranquilliser; cerebroprotective; neuroprotective; nootropic;
 KW ophthalmological; dermatological; coagulant; cardiant.
 XX
 OS Mus musculus.
 XX
 PN US2002177193-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-MAY-2002; 2002US-00139583.
 XX
 PR 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 98US-0142578P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2003-328485/31.
 DR N-PSDB; ABX93182.
 XX
 PT New isolated zvegfg3 polypeptide, useful for treating cancer, Alzheimer's
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
 PT thrombosis, comprises growth factor domain and CUB domain.
 XX
 PS Claim 1; Fig 6; 73pp; English.
 XX
 CC The present invention relates to the isolation of a growth factor
 CC homologue referred to as zvegfg3, and the polynucleotide sequence encoding
 CC it. The zvegfg3 polypeptide is useful for stimulating the growth of
 CC fibroblasts or smooth muscle cells, or for activating a cell-surface
 CC platelet-derived growth factor (PDGF) alpha receptor. The zvegfg3
 CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
 CC for treating full-thickness skin wounds, female reproductive tract and
 CC prolonged bleeding, periodontal disease, damaged liver tissue, and
 CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
 CC adhesives for promoting revascularisation of healing tissue. The zvegfg3
 CC polypeptide is also useful for treating liver damage including damage due
 CC to liver disease, chronic active hepatitis, hepatic chronic passive
 CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein

CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
 CC cirrhosis. The polypeptide is useful for enhancing expansion and
 CC mobilisation of endothelial precursor stem cells, creating and
 CC stabilising new vessel formation in areas requiring neovascularisation,
 CC including areas of ischaemia, organ transplants, wound healing, and
 CC tissue grafting. It may be used for treating peripheral neuropathies by
 CC increasing spinal cord and sensory neurite outgrowth, and as part of
 CC therapeutic treatment for the regeneration of neurite outgrowths
 CC following strokes, brain damage caused by head injuries, and paralysis
 CC caused by spinal injuries. Application may also be made in treating
 CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
 CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
 CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
 CC zvegfg3 is useful for blocking the mitogenic, chemotactic, or angiogenic
 CC effects of zvegfg3, and for treating proliferative vascular disorders,
 CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
 CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
 CC and diseases of the nervous system. The present sequence represents mouse
 CC zvegfg3

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3e-181;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLSSDKQGVQDPRHRVVTISGNGSIHS 60
 DB 1 MLLGLLLLTALAGORTGTRAESNLSSKQLSSDKQGVQDPRHRVVTISGNGSIHS 60
 QY 61 PKFHTYPRNNVLVRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
 DB 61 PKFHTYPRNNVLVRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
 QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDYFPSPGFCIHYSIIMPQVTTTSPSLPSS 180
 DB 121 GRWCGSGTVPKGKTSKGNHIRFVSDYFPSPGFCIHYSIIMPQVTTTSPSLPSS 180
 QY 181 LSLDLLNNAVTAFTLEELIRYLPDRQVOLDLSLYKETWOLLGKAFLYGKSKVVNLLNL 240
 DB 181 LSLDLLNNAVTAFTLEELIRYLPDRQVOLDLSLYKETWOLLGKAFLYGKSKVVNLLNL 240
 QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
 QY 301 VTKKYHEVLQRLPKTGVKGLHKSITDVALEHHEBCDCVCRGNAGG 345
 DB 301 VTKKYHEVLQRLPKTGVKGLHKSITDVALEHHEBCDCVCRGNAGG 345

RESULT 10

ADG47752
 ID ADG47752 standard; protein; 345 AA.

XX
 AC ADG47752;

DT 11-MAR-2004 (first entry)

DE Mouse zvegfg3 protein.

KW Vulnerary; dermatological; wound healing; proliferation; zvegfg3.; mouse.

OS Mus musculus.

PN US6528050-B1.

PD 04-MAR-2003.

PF 06-NOV-2000; 2000US-00706968.

PR 07-DEC-1998; 98US-0111173P.

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PR 06-JUL-1999; 99US-0142576P.
PR 21-OCT-1999; 99US-0161653P.
PR 12-NOV-1999; 99US-0165253P.
PR 07-DEC-1999; 99US-00457066.
PR 31-MAR-2000; 2000US-00541752.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
XX
XX WPI; 2003-370630/35.
XX N-PSDB; ADG47751.
XX
XX Promoting wound healing or proliferation of fibroblasts or smooth muscle
XX cells in a mammal, by administering a polypeptide comprising growth
XX factor domain of human growth factor homolog polypeptide, zvegfg3.
XX
XX Disclosure; SEQ ID NO 43; 69pp; English.
XX
XX The present invention relates to a method of promoting wound healing,
XX especially a dermal wound and for promoting proliferation of fibroblasts
XX or smooth muscle cells in a mammal, by administering a polypeptide
XX comprising growth factor domain of human growth factor homolog
XX polypeptide, zvegfg3. The present sequence is mouse zvegfg3 protein.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 1848; DB 7; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
QY 61 PKFPHYPRNMVWLWRLVAVDENVRILTDFERFGLDEPDDEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNMVWLWRLVAVDENVRILTDFERFGLDEPDDEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
DB 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEEDCDVCVRNAGG 345
DB 301 VTKKYHEVLQRLPKTGKGLHLSLTDVALEHHEEDCDVCVRNAGG 345
RESULT 11
ADJ32788
ID ADJ32788 standard; protein; 345 AA.
XX
XX AC ADJ32788;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Mouse zvegfg3 protein.
XX
XX Growth factor homologue; zvegfg4; skin wound; venous stasis; ulcer;
XX fracture repair; skin grafting; neovascularisation;
XX female reproductive tract disorder; bleeding; gastrointestinal tract;
XX liver damage; hepatic chronic passive congestion; CPC;
XX central haemorrhagic necrosis; CHN; neurite growth; neuropathy;
XX neurodegenerative disease; multiple sclerosis; Alzheimer's disease;
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KW Parkinson's disease; cell proliferation; cancer; gene therapy; mouse.
XX Mus sp.
XX US2004002140-A1.
XX 01-JAN-2004.
XX
XX 06-JUN-2001; 2001US-00876813.
XX
XX 03-MAY-1999; 99US-0132250P.
XX 10-NOV-1999; 99US-0164463P.
XX 04-FEB-2000; 2000US-0180169P.
XX 03-MAY-2000; 2000US-00564595.
XX
XX (GILB/) GILBERT T.
XX (HART/) HART C E.
XX (SHEP/) SHEPPARD P O.
XX (GILB/) GILBERTSON D G.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
XX WPI; 2004-070738/07.
XX N-PSDB; ADJ32787.
XX
XX New zvegfg4 polypeptides and nucleic acids, useful for diagnosing or
XX treating cell loss or abnormal cell proliferation, e.g. cancer, treating
XX full-thickness skin wounds or treating female reproductive tract
XX disorders.
XX
XX Disclosure; SEQ ID NO 35; 73pp; English.
XX
XX The invention relates to growth factor homologue zvegfg4, its
XX corresponding nucleic acid and methods of using them. The sequences of
XX the invention are used in the study and regulation of cell and tissue
XX development, as components of cell culture media and as diagnostic
XX agents. The zvegfg4 polypeptide can be used in treating full-thickness
XX skin wounds, including venous stasis, ulcers and other chronic, non-
XX healing wounds, in fracture repair, skin grafting, in constructive
XX surgery to promote neovascularisation and increase skin flap survival, to
XX establish vascular networks in transplanted cells and tissues, or in
XX treating female reproductive tract disorders, including acute or chronic
XX placental insufficiency and prolonged bleeding. It can also be used to
XX promote endothelialisation of vascular grafts and stents, in treating
XX acute or chronic lesions of the gastrointestinal tract or treating or
XX repairing liver damage. Zvegfg4 can also be used for treating hepatic
XX chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
XX zvegfg4 proteins, agonists and antagonists can also be used to modulate
XX neurite growth and development and demarcate nervous system structures.
XX It can also be used for treating peripheral neuropathies or
XX neurodegenerative diseases including multiple sclerosis, Alzheimer's
XX disease or Parkinson's disease. The polypeptides, nucleic acids and
XX antibodies can also be used to diagnose or treat disorders associated
XX with cell loss or abnormal cell proliferation (including cancer). The
XX invention is useful in gene therapy. The present sequence is mouse zvegfg3
XX protein.
XX
XX Sequence 345 AA;
SQ
Query Match 100.0%; Score 1848; DB 8; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLLTSAAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60
QY 61 PKFPHYPRNMVWLWRLVAVDENVRILTDFERFGLDEPDDEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNMVWLWRLVAVDENVRILTDFERFGLDEPDDEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
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Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 12
ADL18359
ID ADL18359 standard; protein; 345 AA.
XX ADL18359;
AC ADL18359;
XX 20-MAY-2004 (first entry)
DT Mouse zveg3 protein.
DE Bone; ligament; cartilage; growth; mouse; zveg3; proliferation;
XX Bone differentiation; osteoblast; osteoclast; chondrocyte;
KW bone marrow stem cell.
KW Mus musculus.
OS
FH Key
FT Region
FT 235..345
FT /note= "Specifically claimed in Claim 1"
XX US2004043031-A1.
XX 04-MAR-2004.
XX 19-SEP-2003; 2003US-00664432.
XX 07-DEC-1999; 98US-00457056.
PR 31-MAR-2000; 2000US-0193723P.
PR 29-MAR-2001; 2001US-00823033.
XX (Zymo) ZYMOGENETICS INC.
PA Hart CE, Gilbertson DG;
PI WPI; 2004-303322/28.
DR N-PSDB; ADL18358.
XX Promoting growth of bone, ligament or cartilage in mammal involves
PT administering to mammal composition comprising zveg3 dimeric protein and
PT delivery vehicle.
XX Claim 1; SEQ ID NO 4; 31pp; English.
XX The present invention relates to methods for promoting bone, ligament or
CC cartilage growth in a mammal. The methods involve administering to the
CC mammal a composition comprising a dimeric protein of human or mouse
CC zveg3 sequence and a delivery vehicle. Also disclosed are methods for
CC promoting proliferation or differentiation of osteoblasts, osteoclasts,
CC chondrocytes, or bone marrow stem cells. The delivery vehicle is powdered
CC bone, tricalcium phosphate, hydroxyapatite, polymethacrylate, or
CC biodegradable polyester, aqueous polymeric gel or fibrin sealant. The
CC methods of the invention are useful for promoting growth of bone,
CC ligament or cartilage in a mammal. The present sequence represents mouse
CC zveg3 protein.
XX Sequence 345 AA;
SQ Query Match 100.0%; Score 1848; DB 8; Length 345;

Best Local Similarity 100.0%; Pred. No. 3e-181;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGORTGTRAENSLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLTTSALAGORTGTRAENSLSSKQLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
QY 61 PKPHTYPRNNMVLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPHTYPRNNMVLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRLPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
RESULT 13
AA41766
ID AA41766 standard; protein; 345 AA.
XX AA41766;
XX 07-DEC-1999 (first entry)
XX Human PRO200 protein sequence.
DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX Homo sapiens.
OS WO9946281-A2.
FN 16-SEP-1999.
PD 08-MAR-1999; 99MO-US005028.
PF 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
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PR 27-MAR-1998; 98US-0079728P.
PR 30-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 31-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080322P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
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PR 08-APR-1998; 98US-0081049P.
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PR 09-APR-1998; 98US-0081193P.
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PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081953P.
PR 21-APR-1998; 98US-0082568P.
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PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083493P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
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PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH) GENENTECH INC.
XX
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
DR N-PSDB; AAZ34296.
XX

PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX Claim 12; Fig 207; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAZ41685 to
CC AAZ41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Fred. No. 1.4e-162;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
DB 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVQDQHERIITVSTNGSIHS 60
QY 61 PKFPHTYPRNMVLMVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
DB 61 PRFPHTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSEPGFCIHYNLVMPPQFTEAVSPSVLPSSA 180
QY 181 LSLDLLANNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGAFLYKSKKYVNLNL 240
DB 181 LPLDLLANNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGAFLYKSKRVVDNLNL 240
QY 241 LKEEVKLYSCTPRNFPSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
DB 241 LTEEVRLYSCTPRNFPSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEEDCDVCRCNAGG 345
DB 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEEDCDVCRCSTGG 345

RESULT 14
AAV30023
ID AAV30023 standard; protein; 345 AA.
XX
AC AAV30023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
KW Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
XX
PN WO9937671-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US001574.
XX
PR 27-JAN-1998; 98US-0072635P.
PR 05-JUN-1998; 98US-0080899P.
PR 24-JUN-1998; 98US-0090544P.

PR 31-AUG-1998; 98US-0098548P.
XX (ELIL) LILLY & CO ELI.
XX PI
XX Dou S, Na S, Song HY;
XX
XX WPI; 1999-458680/38.
XX DR N-PSDB; AAX86352.
XX
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding compounds.
PT
XX
XX Claim 1; Page 56-58; 62pp; English.

XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding
CC sequence can be used for the recombinant production of the VEGF-R protein
XX
SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.4e-162;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
DB 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNMVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
DB 61 PRFPHYPRNTVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLDLNNAVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYKSKSVNLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFYKSKSVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKLSTDLVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKLSTDLVALEHHEECDCVCRGNAGG 345

RESULT 15
AAY33679
XX AAY33679 standard; protein; 345 AA.
ID
AC AAY33679;
XX
XX 11-JAN-2000 (first entry)
DT
XX
DE Human VEGF-E protein.
KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping.
XX
OS Homo sapiens.
XX
FN W09947677-A2.

XX 23-SEP-1999.
XX
XX 10-MAR-1999; 99WO-US005190.
XX
XX 17-MAR-1998; 98US-00040220.
XX PR 02-NOV-1998; 98US-00184216.
XX
XX (GETH) GENENTECH INC.
XX
XX Ferrara N, Kuo SS;
XX
XX WPI; 1999-580306/49.
XX DR N-PSDB; AAZ23691.
XX
XX New growth factor polypeptide useful for treating cardiovascular or
PT endothelial disorders, e.g. cardiac hypertrophy.
PT
XX
XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
CC therapeutically, especially by expressing encoding polynucleotides, to
CC treat cardiovascular or endothelial disorders in mammals, especially
CC humans. It is useful in wound repair and tissue generation and
CC regeneration, and may especially be used to treat cardiac hypertrophy It
CC can be combined with a carrier in pharmaceutical compositions, which can
CC be administered to treat disorders as above. VEGF-E can be used to screen
CC for antagonists and agonists, and the antagonists administered to treat
CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-
CC related macular degeneration. It can be used to generate antibodies,
CC useful therapeutically as antagonists, as above. The antibodies are also
CC useful to detect VEGF-E polypeptide, especially to diagnose
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
CC vascular disease, or neovascularization associated with tumor formation),
CC by contacting the antibody with a tissue sample and detecting formation
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-
CC E can be used to diagnose cardiovascular and endothelial disorders in
CC mammals, by detecting abnormally high or low VEGF-E gene expression in
CC tissue samples. They can also be used to diagnose a disease or
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
CC sample. They may also be used to produce probes useful to detect related
CC sequences or for gene mapping. This sequence represents the human VEGF-E
CC protein described in the method of the invention
XX

SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.4e-162;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVITSGNGSIHS 60
DB 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQFSSNKQNGVQDPOHERIITVSTNGSIHS 60
QY 61 PRFPHYPRNMVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
DB 61 PRFPHYPRNTVLRVAVDENVRIQLTFDERFGLDEPDDEICKYDFVEEPEPSDGSVL 120
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSPSEPGFCIHYSIIMPQVTTTSPSLPPSS 180
QY 181 LSLDLNNAVAFSTLEELIRYLPDRQVLDLSLYKPTWQLLKAFYKSKSVNLNL 240
DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLKAFYKSKSVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300

Qy 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHHECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHHECDCVCRGSTGG 345

Search completed: September 3, 2005, 19:25:51
Job time : 122.5 sec8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:17:40 ; Search time 25.5 Seconds
(without alignments)
1301.756 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	40.8	370	2	JC7592
2	753	40.7	370	2	spinal cord-derive
3	746.5	40.4	370	2	JC7998
4	191	10.3	707	2	JC2218
5	190	10.3	823	1	A58788
6	183.5	9.9	927	1	JQ0948
7	183.5	9.9	927	1	BMH01
8	181	9.8	986	1	B58788
9	181	9.8	991	2	I49540
10	174.5	9.4	3623	2	T09456
11	160	8.7	3623	2	T08618
12	158	8.5	449	2	A53362
13	153	8.3	1057	1	A39288
14	147.5	8.0	1524	2	T30337
15	145.5	7.9	686	1	A59271
16	144	7.8	699	1	I54763
17	143.5	7.8	597	2	S71352
18	141.5	7.7	1070	2	T31069
19	140.5	7.6	3871	2	T22812
20	139	7.5	1594	2	T30549
21	137.5	7.4	705	1	CHURB
22	135.5	7.3	1464	2	S58984
23	133.5	7.2	4002	2	JH0403
24	128	6.9	277	2	A41735
25	127	6.9	419	2	S69207
26	126.5	6.8	579	2	JC7629
27	125.5	6.8	245	1	TVC2SS
28	125.5	6.8	767	2	J30018
29	125	6.8	533	2	JC7985

30 123 6.7 275 2 JC6506 tumor necrosis fac
31 122.5 6.6 2403 2 A59386 sanko - human
32 119.5 6.5 2083 2 T42721 CRP-ductin-alpha p
33 117.5 6.4 276 2 A47290 TSG-6 homolog PS4
34 117.5 6.4 1290 2 A57190 ebnerin precursor
35 114.5 6.2 200 2 I51551 platelet-derived g
36 114.5 6.2 215 2 S08220 platelet-derived g
37 114.5 6.2 226 2 I51550 platelet-derived g
38 113 6.1 695 1 S05008 complement subcomp
39 112.5 6.1 241 1 PFHUG2 platelet-derived g
40 111.5 6.0 226 1 TVMVSS PDGF-related trans
41 109 5.9 694 2 JC6554 complement subcomp
42 108.5 5.9 148 2 D49530 16K vascular endot
43 107 5.8 321 2 T33161 hypothetetical prote
44 104 5.6 319 2 I51569 UVS.2 protein - Af
45 103.5 5.6 225 2 S25097 platelet-derived g

ALIGNMENTS

RESULT 1
JC7592
spinal cord-derived growth factor-B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7592
R:Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170
C:Genetics:
A:Gene: scdgf-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

Query Match	40.8%	Score 754;	DB 2;	Length 370;
Best Local Similarity	46.2%	Pred. No. 8.2e-55;		
Matches 151;	Conservative 62;	Mismatches 86;	Indels 28;	Gaps 10;
Qy	37 EQNGVQD-PRHRRVVTISNGSIHSKPFPHYPRNMLVWRLVAVDENVRITQTFDERFG	95		
Db	42 ESNHLDLYRRDENIRVTGTGHVQSPRFPNSYPRNLLTWRLHS-QEKTRIQLAFDHQFG	100		
Qy	96 LEDPEDIKDYFVEVEPEPSDGS--VLGRWCGSGTVPGKQTSKGNHPIRFVSEYFPSE	153		
Db	101 LEEAENICRYDFVEVEDVSESSTVVRGWCGHKHEIPRITSRTNQIKITFQSDDYFVAK	160		
Qy	154 PGFCHYSII---MPQ-----VTET-----TSPSLPPSSLSLDLNNNAVTAFTST	195		
Db	161 PGFKIYTSFVEDFQFEAAEINWESVTSFSGVSYHSPSVM-DSTLTADADKAIAEDT	219		
Qy	196 LEEIRYLEPDRWQVLDLSLYKPTWQLLGKAFKYGKSKVYNLNLKKEVKLYSCTPRNF	255		
Db	220 VEDLLKYFNPASWQDLENLVMDTPRYGRSY-HERKSK-VDLRLNDDVKRYSCTPRNH	277		
Qy	256 SVSTRBELKRTDTTFWPGCLLVKCGGNCACCLHNCQCQPRKYVTKYHEVLQLRP--	313		
Db	278 SWNLREELKLTNAVFPFRCLLVQRCGGCGTLNWKSCCTSSGKTVKXKHYEVLKFEFGH	337		
Qy	314 -KTGVKGLHSLTDVALEHHEECDCVC	339		
Db	338 FRRGKAKMALVDIQDHHERCDCIC	364		

```

RESULT 2
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7591
R:Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280: 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C:Genetics:
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor
F:294-308/Region: conserved motif #status predicted

Query Match 40.7%; Score 753; DB 2; Length 370;
Best Local Similarity 45.3%; Pred. No. 9.9e-55;
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

QY 37 EQNGVQD-PRHVVVTISNGSIHSPKPHPTYPNNMLVWLVAVDENVRIQLTFDERPG 95
DB 42 ESNHLTDLYRDETQVKGNGVQSPFPNSYPNNLLTWRLHS-QENTRIQLVDFNOFG 100
QY 96 LEDPDDICKYDFVVEEPESDGSLV--GRWCGSGVPGKQTSKGNHRIKRVSDYFVPS 153
DB 101 LBEAENDICRYDFVEVEDISESTIIRGWGHEKVPRIKRTQIKITFKSDDYFVAK 160
QY 154 PGFCIHYSII---MPQVTETT-----SPSVLPSSLSLDDLNNAVTAFST 195
DB 161 PGFKIVYSLLDFQPAASSETNWESVTSISGVSNPSVTDTP-TLIADALDKKIAEFD 219
QY 196 LBEILRYLEPDWQVLDLSLYKPTWQLLGKAFLYKKSKVNNLLKEEVKLYSCTPRNF 255
DB 220 VDLRLKYFNPESQWQDENLNYLDTPTRYGRSY-HSRKSK-VDLRLNDNDKRYSCPT 277
QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRKVTYKHYEVLQLRP-- 313
DB 278 SVNIREELKLANVFPFRCCLLVQRCGNCCTVNRSTCNSGKTVKHYEVLQFEPGH 337
QY 314 -KTGVKGLHKSITDVALEHHEECDCVC 339
DB 338 IKRRGRKTMALVDIQLDHHERCDCIC 364

RESULT 3
JC7998
platelet-derived growth factor-D - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C:Accession: JC7998
R:Zhao, Y.; Hoyie, G.W.; Zhang, J.; Morris, G.; Lasky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A:Title: A novel murine PDGF-D splicing variant results in significant differences in pe
A:Reference number: JC7998; PMID:12890490
A:Accession: JC7998
A:Molecule type: mRNA
A:Residues: 1-370 <ZHU>
C:Comment: This protein is a potent mesenchymal cell mitogen and chemoattractant involve
C:Genetics:
A:Gene: pdgf-D
A:Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C:Keywords: fibrosis; PDGF-D

Query Match 40.4%; Score 746.5; DB 2; Length 370;
Best Local Similarity 43.5%; Pred. No. 3.4e-54;
Matches 151; Conservative 63; Mismatches 102; Indels 31; Gaps 9;

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QY 16 QRTGTRAESNLSSKLQSSDKQNGVQDPRHVVVTISNGSIHSPKPHPTYPNNMLVW 75
DB 26 QRASIKALRNAN-----LRRDESNLHLDLYQREENIQVTNSNGHVQSPFPNSYPNNLLTW 81
QY 76 RLVAVDENVRIQLTFDERFGLDEPDDICKYDFVVEEPESDGSLV--GRWCGSGVPGKQ 133
DB 82 WLRS-QEKTRIQLSDFDQFGLBEAENDICRYDFVVEEVEVSSSTVVRGWCGHKEIPRI 140
QY 134 TSKGNHRIKRVSDYFVVEEPESGFCIHYSII---MPQVTETT-----SPSV 175
DB 141 TSRTNQIKITFKSDDYFVAKDPGFKIYTSFVEDFQPEAASSETNWESVTSFSGVSVHSPSI 200
QY 176 LPPSSLSLDDLNNAVTAFSTLEELIRYLEPDWQVLDLSLYKPTWQLLGKAFLYKKSKV 235
DB 201 TDP-TLTADALDKTVAEPTVDELTKHFNPNVSWQDDLENLYLDTPTHYGRSY-HDRKSK- 257
QY 236 VNLMLKEEVKLYSCTPRNFVSIREELKRYDTTFWPGCLLVKRCGNCACCLHNCNECQ 295
DB 258 VDLRLNDNDKRYSCPTPRNHSVNLREELKLTNAVFFPRCLLVQRCGNCCTVNRWKSCT 317
QY 296 CVPRKVTYKHYEVLQLRP---KTGVKGLHKSITDVALEHHEECDCVC 339
DB 318 CSSGKTVKHYEVLKFEFGHFRKRGKAKNMALVDIQLDHHERCDCIC 364

RESULT 4
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N:Alternate names: bone morphogenic protein 1
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JC2218
R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A:Reference number: JC2218; MUID:94085787; PMID:8262384
A:Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; E
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: astacin homology <AST>
F:285-397/Region: complement 1r/1s-like repeat
F:285-394/Domain: Clr/Cls repeat homology <Clr1>
F:398-510/Region: complement 1r/1s-like repeat
F:398-507/Domain: Clr/Cls repeat homology <Clr2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement 1r/1s-like repeat
F:554-663/Domain: Clr/Cls repeat homology <Clr3>
F:62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.3%; Score 191; DB 2; Length 707;
Best Local Similarity 45.2%; Pred. No. 9.7e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHPTYPNNMLVWLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEE- 113
DB 562 NGSINSPGWPKYPPNNKNCIQLVAPTO-YRISLKFDQ---FETEGNDVCKYDFVEVRSG 617
QY 114 -PSDGSVLGRWCGSGVPGKQTSKGNHRIKRVSDYFVPSPPGF 156
DB 618 LTSDSKLHGKFCGS-ELPAVITSVNNMRIFBKSDNTV-SKKGF 659

RESULT 5
A58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human

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N:Alternate names: bone morphogenic protein splice form BMP-1/His
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; A58788
R:Woźney, J.M.; Rosen, V.; Celeste, A.J.; Mitscock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EXPPALQPRGRPHQLKFRVQKNTPTQ' <WO2>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encod
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:738-752/Region: histidine-rich
F:91.142,332,363,599/Binding site: carbohydate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 10.3%; Score 190; DB 1; Length 823;
Best Local Similarity 36.0%; Pred. No. 1.4e-07;
Matches 54; Conservative 20; Mismatches 48; Indels 28; Gaps 7;

Qy 55 NGSIHSPKFPHTYPRNMVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKEYPPNKNCIWQVAPQO-YRISLQFD---FFTEGNDVCKYDFVEVRSG 654

Qy 114 -PSDGSVLGRWCGSGTVPKQTSKGNHIRIRFVSDEYPPSPGFCIHV----- 160
Db 655 LTADSKLHGKFCGS-EKPEVITSQYNNMRVFKSDNTV-SKKGPKAHFVSLEGAGDRHS 712

Qy 161 -----SIIMQVTTTSPVLPSLSLD 184
Db 713 HLSGLELLCPHALVDTPVA--PPSALHGD 740

RESULT 6
BMHUI
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
N:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: A37278; E58788
R:Woźney, J.M.; Rosen, V.; Celeste, A.J.; Mitscock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-730 <WO2>

A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
C:Genetics:
A:Gene: GDB:BMP1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-823/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:91.142,332,363,599/Binding site: carbohydate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.9%; Score 183.5; DB 1; Length 730;
Best Local Similarity 38.9%; Pred. No. 4.2e-07;
Matches 49; Conservative 18; Mismatches 44; Indels 15; Gaps 6;

Qy 55 NGSIHSPKFPHTYPRNMVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKEYPPNKNCIWQVAPQO-YRISLQFD---FFTEGNDVCKYDFVEVRSG 654

Qy 114 -PSDGSVLGRWCGSGTVPKQTSKGNHIRIRFVSDEYPPSPGFCIHVSIIMQVTTTTS 172
Db 655 LTADSKLHGKFCGS-EKPEVITSQYNNMRVFKSDNTV-SKKGPKAHF-----FSEKR 705

Qy 173 PSVLPP 178
Db 706 PALQPP 711

RESULT 7
JQ0948
A5 antigen precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JQ0466; JQ0948
R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
A:Reference number: JQ0466; MUID:91337458; PMID:1908252
A:Accession: JQ0466
A:Molecule type: mRNA
A:Residues: 1-927 <TAK>
A:Cross-references: GB:D10467; GB:D01077; NID:G2222962; PIDN:BA001260.1; PID:G222963
A:Experimental source: tadpole, brain
A:Note: This protein has motifs homologous to complement components C1r and C1s and to c
C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal rec
C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-927/Product: A5 antigen #status predicted <ASA>
F:27-138/Domain: C1r/C1s repeat homology <C1R1>
F:147-262/Domain: discoidin I amino-terminal homology <C1R2>
F:274-424/Domain: discoidin I amino-terminal homology <DNI>
F:430-584/Domain: discoidin I amino-terminal homology <DN2>
F:646-812/Domain: MAM homology <MAM>
F:861-883/Domain: transmembrane #status predicted <TMAM>
F:150,261,300,523,844/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 183.5; DB 1; Length 927;
Best Local Similarity 30.7%; Pred. No. 5.7e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

Qy 50 VTISNGSIHSPKFPHTYPRNMVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFV 109

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Db 31 IKITSPSLTSGYSHSPPSORCEMLQAEHYQRIMNPNPHDLEDR---CKIDYV 87
QY 110 EV--EERSDGVLGRWCSSGTVPGKQTSKGNHIRIRFVDSYFVSEPGFCIHYSIIM--P 165
Db 88 EVIDGDNAGQLLKGKCGK-IAPSPLVSTGSPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145
QY 166 QVTE--TWTSPSLP-----PSSLSDLLNNAVTAFTLEELIRVLEPDRMQVDLDS 214
Db 146 ECSRNFTSSNGVIKSPKPYKPNALCTYIFA-----PRMQEIV--LEFSSFELEADS 198

RESULT 8
B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N:Alternate names: bone morphogenic protein 1, tolloid-like splice form
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C:Accession: A37278; B58788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKRPALQPPRGPHQLKFRVQKNRTPQ' <WOZ>
A:Cross-references: UNIPROT:P13497; GB:W22486; NID:gl79499; PIDN:AAA51833.1; PID:gl79500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encod
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TAK>
A:Cross-references: GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g619861
C:Genetics:
A:Gene: GDB:BMPL; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
A:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:223-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:91-142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.8%; Score 181; DB 1; Length 986;
Best Local Similarity 42.6%; Pred. No. 9.9e-07;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 55 NGSIHSPKPHPTYPNNMLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE- 113
Db 599 NGSITSPGWPKEYPNNKNCIWLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
QY 114 -PSDGSVLGRWCSSGTVPGKQTSKGNHIRIRFVDSYFVSEPGFCIH 160
Db 655 LTADSKLHGKFCGS-EKPEVITSQNNMRVEFKSDNTV-SKKGFKAHF 700

RESULT 9
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149540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I49540; MUID:94229342; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: hydrolase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

Query Match 9.8%; Score 181; DB 2; Length 991;
Best Local Similarity 42.6%; Pred. No. 1e-06;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 55 NGSIHSPKPHPTYPNNMLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE- 113
Db 604 NGSITSPGWPKEYPNNKNCIWLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 659
QY 114 -PSDGSVLGRWCSSGTVPGKQTSKGNHIRIRFVDSYFVSEPGFCIH 160
Db 660 LTADSKLHGKFCGS-EKPEVITSQNNMRVEFKSDNTV-SKKGFKAHF 705

RESULT 10
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09456
R:Kozyraki, R.; Kristsianen, M.; Silahataroglu, A.; Hansen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A:Reference number: Z16677; MUID:98241400; PMID:9572993
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-3623 <KOZ>
A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3
C:Genetics:
A:Map position: 10p12
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 9.4%; Score 174.5; DB 2; Length 3623;
Best Local Similarity 31.9%; Pred. No. 1.8e-05;
Matches 53; Conservative 26; Mismatches 64; Indels 23; Gaps 8;
QY 15 QORTGTAEENLSSK-----LQLSSD--KEQGVQDPRHERVVTISGNNGSIH----- 59
Db 2173 GHFCGSHASSTLFTSDNQMFQVIFSDHSNEQGQFKIYEAKSLACGGNVYIHDAASGYV 2232
QY 60 -SPKFPHTYPNNMLVRLVAVDENVRIQLTFDERFGLEDDEDDICKYDFVEVEE--PSD 116
Db 2233 TSPNHPHNPYPHADCIWILAAPPE-TRIQLQFEDRFDIETPN--CTSNYLELRDGVDS 2289
```

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QY 117 GSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEFSGFCIHYSI 162
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 2290 ABILSKFCGT-SLPSSQSSGGEVYLRPSDN-SPTHVGFKAQYSI 2333
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

RESULT 11
T08618
C:Keywords: intrinsic factor-B12 receptor CUBILIN precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08618
R:Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Braut,
J. Biol. Chem. 273, 5235-5242, 1998
A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A:Reference number: Z16459; MUID:98148073; PMID:9478979
A:Accession: T08618
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3623 <MOE>
A:Cross-references: UNIPROT:070244; EMBL:AF022247; NID:G3834379; PIDN:AAC71661.1; PID:G3
C:Genetics:
A:Gene: CUBILIN
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F:133-164/Domain: EGF homology <EGF>
F:436-467/Domain: EGF homology <EGF>

Query Match 8.7%; Score 160; DB 2; Length 3623;
Best Local Similarity 26.8%; Pred. No. 0.00028;
Matches 90; Conservative 44; Mismatches 130; Indels 72; Gaps 23;

QY 31 QLSSDKEQGVQDPHREHVVITSGNSIHSPKFTYPRNMVLVRLVAVDENVRIQLTF 90
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 924 KPSDDKLCG-----EVLTA-SGIIESGPHNVPYRGVNCVTHVV-VORGQILRLEF 974
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 91 DERFGLPEDDICKYDFVEEPEBDSGVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYF 150
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 975 SS-FYLEFHYN--CTNDVLEIYDTAAQTLGKYCGK-SIPPSLTSNSIKLIFVSDSAL 1030
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 151 PSEPGFCIH-----STIMPOVTT-----TSPSVLP---PSS-----LSLDLNNAVT 191
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1031 AHE-GFSINYEAIDASSVCLVYDNTDFNGMLSPN-FPNYPSPNWCIVRIITVGLNQIAL 1088
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 192 AFS--TLSEELRYLPRDQVLDLSLYKFTWQLLQKAFYGGKSKVNLNLLKEEVKLY- 248
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1089 HFTDFTLEDYFGSQCVDFVEI-RDGGYE-TSLVVG---IY--CGSVLPPTIISHSNKLWL 1141
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 249 -----SCTPRNFVSISIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEQCQVPRKVT 302
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1142 KFKSDAALTAKGFS-----YWDGS--STGCGN-----LTPTGVLTPSPNYPM 1183
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 303 KKYHE---VLQLRPKTVGKGLHKSITDVALBHEEC 335
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1184 PYTHSSECYWRLEASHG-SPELEFQDFLHHPSC 1218
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

RESULT 12
A55362
procollagen I C-proteinase enhancer protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 15-Mar-2004
C:Accession: A55362
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show
J. Biol. Chem. 269, 26280-26285, 1994
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p
A:Reference number: A55362; MUID:95014462; PMID:7523404
A:Accession: A55362
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TAK>
```

```
A:Cross-references: GB:L33799; NID:G642907; PIDN:AAA61949.1; PID:G642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: C1r/C1s repeat homology <C1r1>
F:159-270/Domain: C1r/C1s repeat homology <C1r2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,431/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 8.5%; Score 158; DB 2; Length 449;
Best Local Similarity 34.5%; Pred. No. 3e-05;
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

QY 56 GSIHSPKFPHT-YPRNMVLVRLVAVDENVRIQLTFDERFGLPEDDICKYDFVEV--- 111
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 168 GTLTTPNWPESDYPFGISCSWHIIAPPDQV-IALTFF-EKFDLE--PDYCYRDSVSVFNG 223
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 112 EEPDSGVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEFSGFCIHYSIIM----- 164
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 224 AVSDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 165 --PQVTTETSPV-LPPSS 180
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 282 QGPGPKRGTEPKVKLPKPS 300
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

RESULT 13
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanoga
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
C:Genetics:
A:Gene: FlyBase:tlid
A:Cross-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repe
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1r1>
F:468-578/Domain: C1r/C1s repeat homology <C1r2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <C1r3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <C1r4>
F:900-1013/Domain: C1r/C1s repeat homology <C1r5>
F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.3%; Score 153; DB 1; Length 1057;
Best Local Similarity 33.3%; Pred. No. 0.00023;
Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;

QY 13 LAGQRTGTRAESNLSKQLQSSDKQGVQDPHRRV-----VTISGNGSIHSPKFPHTYP 68
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 432 VSGEVIITQTSRMLLVNVRNAAGYRGFK-ARPEVVCVGGDLTKDQSIDSPNYPMDYM 490
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 69 RNMLVRLVAVDENVRIQLTFDERFGLPEDDICKYDFVEVE--PSDCSVLGRWCGS 126
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 491 PDKECVIRITAPD-NHQVALKF-QSFELE--KHDGCAVDFVEIRDGNHSDRLIGRFGCD 546
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
```

QY 127 GTPGKQTSKGNHIRFVSD 147
DB 547 KLPPNIKT-RSQMVIKRVSD 566

RESULT 14

T30337
polyprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30337
R:Yang, J.C.; Lindas, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X.
A:Reference number: Z20829
A:Accession: T30337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: UNIPROT:Q91674; EMBL:U01290; NID:G2981640; PID:G2981641; PIDN:AAC247
C:Superfamily: tryosin related polyprotein; trypsin homology

Query Match 8.0%; Score 147.5; DB 2; Length 1524;
Best Local Similarity 28.7%; Pred. No. 0.001;
Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;
QY 56 GSIHSPKFPHTYPRNMVLVAVDENVRIOQLTDERFGLDEPDDICKYDFVEV-BEP 114
DB 439 GMVSPNYPDPYPRLKTCWS-IIIEAPENHIVLKFED-FNVEYGHG--CIYDAVEVYDGA 494
QY 115 SDGVLGRWCGSGTVPKGQTSKGNHIRFVSDYFPPSPGFCIHYSIIIMQ-----VT 168
DB 495 EKKLIARLCGY-TLPLPISSPENTMLIRFKTD-MENSYPGPKVRFSPVPEKQKPSLPVD 552
QY 169 ETPSPVLPPSLSLDLNNA-VTAFSTLEELIRYLEPD-----RMQVDL-----DS 214
DB 553 DPTITSMHLPRALDVCGMAPTQKWLPRIVGGEASPNWPQVQIFFLRTFHCBA 612
QY 215 LYKPTWQL 222
DB 613 IISQWIL 620

RESULT 15

A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laurson, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates d
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:O00187; GB:Y09926; NID:G4007626; PIDN:CAA71059.1; PID:G40076
A:Experimental source: tissue liver
A>Note: submitted to GenBank, December 1996
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: lp36.2-lp36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine P
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1R1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>

F:300-361/Domain: complement factor H repeat homology <FH1>
F:366-430/Domain: complement factor H repeat homology <FH2>
F:445-679/Domain: trypsin homology <TRI>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,58
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 7.9%; Score 145.5; DB 1; Length 686;
Best Local Similarity 30.8%; Pred. No. 0.00055;
Matches 33; Conservative 27; Mismatches 42; Indels 5; Gaps 4;

QY 55 NGSIHSPKFPHTYPRNMVLVAVDENVRIOQLTDERFGLDEPDDICKYDFVEVEEP 114
DB 193 SGELSSPEYPRPYPKLSCTYS-ISLEGFVSVIDFVESFDVETHTLCPYDFLKIQ-- 249
QY 115 SDGVLGRWCGSGTVPKGQTSKGNHIRFVSDYFPPSPGFCIHYS 161
DB 250 TDREHGPFCCK-TLPHRIETKSNVTITFTVDE-SGDHTGKIHYT 294

Search completed: September 3, 2005, 19:30:38
Job time : 26.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:09:34 ; Search time 114.5 Seconds
(without alignments)
1542.946 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
Sequence: 1 MLLGLLLLTALACQRTGT.....DVALEHHBECDVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	2 Q9QY71	Q9QY71 m fallotelin
2	1846	99.9	345	2 Q8C119	Q8C119 mus musculus
3	1819	98.4	345	2 Q9JHV8	Q9JHV8 mus musculus
4	1801	97.5	345	2 Q9EOX6	Q9EOX6 rattus norv
5	1667	90.2	345	2 Q9UL22	Q9UL22 homo sapien
6	1664	90.0	345	2 Q9NRA1	Q9NRA1 homo sapien
7	1552	84.0	345	2 Q91946	Q91946 gallus gall
8	1375	74.4	258	2 Q8K429	Q8K429 rattus norv
9	754	40.8	370	2 Q9BQT1	Q9BQT1 rattus norv
10	752	40.7	370	2 Q9GZP0	Q9GZP0 homo sapien
11	750.5	40.6	364	2 Q9BWV5	Q9BWV5 homo sapien
12	746.5	40.4	370	2 Q9Z517	Q9Z517 mus musculus
13	679.5	36.8	300	2 Q6V9H4	Q6V9H4 oryctolagus
14	440.5	23.8	261	2 Q8K2L3	Q8K2L3 mus musculus
15	201	10.9	923	1 NR1P1	NR1P1 BRARE
16	201	10.9	923	2 Q69DB8	Q69DB8 brachydanio
17	192.5	10.4	691	2 Q57658	Q57658 gallus gall
18	192	10.4	34	2 Q99JM4	Q99JM4 mus musculus
19	191	10.3	707	1 BMP1_XENLA	BMP1_XENLA xenopus lae
20	191	10.3	977	2 Q91925	Q91925 xenopus lae
21	186.5	10.1	871	2 Q6T869	Q6T869 brachydanio
22	186.5	10.1	959	2 Q69DB7	Q69DB7 brachydanio
23	186.5	10.1	959	2 Q6RT22	Q6RT22 brachydanio
24	186.5	10.1	959	2 Q6T870	Q6T870 brachydanio
25	186	10.1	735	2 Q57381	Q57381 xenopus lae
26	186	10.1	735	2 Q66K13	Q66K13 xenopus lae
27	185	10.0	1015	2 Q9Y6L7	Q9Y6L7 homo sapien
28	185	10.0	1078	2 Q9UQ00	Q9UQ00 homo sapien
29	183.5	9.9	928	1 NR1P1_XENLA	NR1P1_XENLA
30	183	9.9	1012	2 Q9WVM6	Q9WVM6 mus musculus
31	181.5	9.8	913	2 Q6NUE0	Q6NUE0 xenopus lae

32	181	9.8	241	2 Q9Z135	Q9Z135 rattus norv
33	181	9.8	775	2 Q6P550	Q6P550 mus musculus
34	181	9.8	986	1 BMP1_HUMAN	BMP1_HUMAN
35	181	9.8	991	1 BMP1_MOUSE	BMP1_MOUSE
36	181	9.8	991	2 Q6NZM2	Q6NZM2 mus musculus
37	176	9.5	538	2 Q6AWA9	Q6AWA9 homo sapien
38	176	9.5	609	2 Q96190	Q96190 homo sapien
39	176	9.5	641	2 Q71SM6	Q71SM6 homo sapien
40	176	9.5	644	2 Q96IH5	Q96IH5 homo sapien
41	176	9.5	704	2 Q9H2E1	Q9H2E1 homo sapien
42	176	9.5	906	2 Q6X907	Q6X907 homo sapien
43	176	9.5	923	1 NR1P1_HUMAN	NR1P1_HUMAN
44	176	9.5	923	2 Q86TS9	Q86TS9 homo sapien
45	175	9.5	923	2 Q68DN3	Q68DN3 homo sapien

ALIGNMENTS

RESULT 1
Q9QY71
ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71.
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Fallotelin (Platelet-derived growth factor C) (Mus musculus adult male
DE cecum cDNA, RIKEN full-length enriched library, clone:9130403008
DE product:platelet-derived growth factor, C polypeptide, full insert
DE sequence) (Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-
DE length enriched library, clone:A730022G11 product:platelet-derived
DE growth factor, C polypeptide, full insert sequence) (Mus musculus 15
DE days embryo head cDNA, RIKEN full-length enriched library,
DE clone:D930001M08 product:platelet-derived growth factor, C
DE polypeptide, full insert sequence).
GN Name=pfgrfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Ovary;
RC Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carrinco P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (KISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF17608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR EMBL; AK033734; BAC28455.1; -.
DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:00050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ Growth factor; Miogen.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 100.0%; Score 1848; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-141;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTCTRAESNLSSKLQLSSDKQNGVDP RHRRVVTISGNGSIHS 60
Db 1 MLLGLLLTSLAGORTCTRAESNLSSKLQLSSDKQNGVDP RHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNWLVRVAVDENVRILQTLTDFERFGLGLED PEDDICKYDFVEVEPSDGSVL 120
Db 61 PKFPHTYPRNWLVRVAVDENVRILQTLTDFERFGLGLED PEDDICKYDFVEVEPSDGSVL 120

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DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 99.9%; Score 1846; DB 2; Length 345;
Best Local Similarity 99.7%; Pred. No. 3e-141;
Matches 344; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
QY 61 PKFPHYTPRNMLVWRLVAVDENVRILTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
DB 61 PKFPHYTPRNMLVWRLVAVDENVRILTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTSLLEIRLYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240
DB 181 LSLDLLNNAVTAFTSLLEIRLYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 3
Q9JHV8 PRELIMINARY; PRT; 345 AA.
ID Q9JHV8;
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=PDGfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during organogenesis.";
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR HSP; Q9JJS8; INTO.
DR MGD; MGI:1859631; Pdgc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . .; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 97.5%; Score 1801; DB 2; Length 345;
Best Local Similarity 96.8%; Pred. No. 1.3e-137;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVODPRHVRVTTISNGSITHS 60
QY 61 PKFPHYTPRNMLVWRLVAVDENVRILTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
DB 61 PKFPHYTPRNMLVWRLVAVDENVRILTDFERFGLDEPDIDCKYDFVEEPEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTSLLEIRLYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240
DB 181 LSLDLLNNAVTAFTSLLEIRLYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 4
Q9EQX6 PRELIMINARY; PRT; 345 AA.
ID Q9EQX6;
AC Q9EQX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=Scdgc;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hanada T., Ue-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033830; BAB19969.1; -.
DR HSP; Q9JJS8; INTO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 2; Length 345;
Best Local Similarity 96.8%; Pred. No. 1.3e-137;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPHRRVVTISNGSIHS 60
DB 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPHRRVVTISNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFTSLLEIRYLEPDRMVDLSIKPTWOLGKAFYLGKSKVNLNL 240
DB 181 LSLDLLNNAVTAFTSLLEIRYLEPDRMVDLSIKPTWOLGKAFYLGKSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Secretory growth factor-like protein fallotenein (Spinal cord-derived
Growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name=hSCDGF; Synonyms=PDGFC; ORFNames=UNQ174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene,
fallotenein, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Rei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -
DR EMBL; AB033831; BAB03266.1; -
DR EMBL; AF260738; AAKS1637.1; -
DR EMBL; AY358493; AAQ88857.1; -
DR HSSP; Q9JJS8; 1INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9B51F40633E78 CRC64;
Query Match 90.2%; Score 1667; DB 2; Length 345;
Best Local Similarity 87.0%; Pred. No. 9.6e-127;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPHRRVVTISNGSIHS 60
DB 1 MSLFGLLLTSALAGORQTOAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60
QY 61 PKPHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
DB 61 PRFHTYPRNMVLRVAVDENVRIOITFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
DB 121 GRWCSGTVPGKQTSKGNHRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSLPSS 180
QY 181 LSLDLLNNAVTAFTSLLEIRYLEPDRMVDLSIKPTWOLGKAFYLGKSKVNLNL 240
DB 181 LPLDLLNNAVTAFTSLLEIRYLEPDRMVDLSIKPTWOLGKAFYLGKSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQRLPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRLPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
RESULT 6
Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Asse K., Karlsson L., Abramson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Besholtz C., Heldin C.-H., Allitalo K., Ostman K., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
receptor.";


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RL Nat. Cell Biol. 2:302-309(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSSP; Q9JJS8; 1NT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 590889CEA55CC5EA CRC64;

Query Match 90.0%; Score 1664; DB 2; Length 345;
Best Local Similarity 86.7%; Pred. No. 1.7e-126;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQGVQDPRHVRVVTISNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRTGTRAESNLSSKFPQSSNKEQGVQDPQHEKIIITVSTNGSIHS 60
QY 61 PKFPHYTPRNMLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGVTL 120
Db 61 PRPPHYTPRNTVLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGVTL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSLPPSS 180
Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHYNIVMQFTFVAVSPSLPPSA 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLN 240
Db 181 LPLDLLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLN 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVRLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGKGLHSLTDVALEHHEEDCDVCRCNAGG 345
Db 301 VTKKYHEVLQLRPKTVGRLHSLTDVALEHHEEDCDVCRCGSTGG 345

RESULT 7
Q9I946 PRELIMINARY; PRT; 345 AA.
AC Q9I946;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=spinal cord;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -.

DR HSSP; Q9JJS8; 1NT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 590889CEA55CC5EA CRC64;

Query Match 84.0%; Score 1552; DB 2; Length 345;
Best Local Similarity 80.3%; Pred. No. 2e-117;
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKEQGVQDPRHVRVVTISNGSIHS 60
Db 1 MLLGLLLLTALAGRRHGAESDLSKFSFPGAKEQGVQDPQHEKIIITVSTNGSIHS 60
QY 61 PKFPHYTPRNMLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGVTL 120
Db 61 PKFPHYTPRNTVLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGVTL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFSPGFCIHYSIIMPQVTTTSPSLPPSS 180
Db 121 GRWCSGTVPGKQIRIRFVSDEYFSPGFCIHYYTLLPHHTFAPSLSLPPSA 180
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLN 240
Db 181 LPLDLLNNAVAFSTVEELIRYLEPDRWQVLDLSLYKPTWQLLKAFYLGKSKVNNLN 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVRLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQIPTK 300
QY 301 VTKKYHEVLQLRPKTVGKGLHSLTDVALEHHEEDCDVCRCNAGG 345
Db 301 VTKKYHEVLQLRPSGVRGLHSLTDVPLEHHEEDCDVCRCNSEG 345

RESULT 8
Q8K429 PRELIMINARY; PRT; 258 AA.
AC Q8K429;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508348; AAM47265.1; -.
DR HSSP; Q9JJS8; 1NT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
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DR PROSITE; PS50278; PDGF 2; 1.
FT NON_TER 1_
FT NON_TER 258 258
SQ SEQUENCE 258 AA; 29255 MW; 86258989FCC3F8B CRC64;

Query Match
Best Local Similarity 74.4%; Score 1375; DB 2; Length 258;
Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 42 QDPRHVVTTISGNSIHSKPKPHYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEPED 101
Db 1 QDPRHVVTTISGNSIHSKPKPHYPRNTVLVWRLVAVDENVRQLTDFDERFGLDEPED 60
QY 102 DICKYDFVEVEPSPGSLGRWCGSGTPGKQTSKGNHIRIRFVDSVEPSPGFCIHYS 161
Db 61 DUCKYDFVEVEPSPGSLGRWCGSGTPGKQTSKGNHIRIRFVDSVEPSPGFCIHYS 120
QY 162 LIIMPQVTTTSPVLPPSPSLSLDLNNAVTAFSTLEELIRLYLEPRWQVLDLSLYKPTWQ 221
Db 121 LIIMPQVTTTSPVLPPSPSALSLLDLNNAVTAFSTVEELIRFLEPRWQVLDLSLYKPTW 180
QY 222 LLGKAFLYGKSKAVNLLKKEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCG 281
Db 181 LLGKAFLYGKSKAVNLLKKEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCG 240
QY 282 GNCACCLHNCNECQCVPR 299
Db 241 GNCACCLHNCNECQCVPR 258

RESULT 9
Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=SCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
Giese N.A., Lokker M.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,
Altalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Iris;
RN MEDLINE=22103462; PubMed=12107412;
RX Wistow G., Barstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
Bouffard G., Smith D., Peterson K.;
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RESULT 12
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AC Q92517: Q9D1L8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Platelet-derived growth factor D (Mus musculus 18-day embryo whole
body cDNA, RIKEN full-length enriched library, clone:1110003109
DE product:platelet-derived growth factor D).
GN Name=Pdgfr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA LaRocheHelle W.J., Jeffers M., McDonald W.P., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deagler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RA "PDGFR D, A Novel Protease-Activated Growth Factor.";
RT Nat. Cell Biol. 3:517-521(2001).
RN [2]
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
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RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Tozawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Arachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335583; AAK38839.1; -
DR EMBL; AK003359; BAB22735.2; -
DR HSSP; Q9JUS8; 1NT0.
DR MGD; MGI:1919035; Pdgfr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
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AC Q8QFX6; Q8AXP1;
STANDARD; FRI;

DB regid protom.
GN Name=Pdgfd;

DB *regu* protein.
GN Name=pdgfd;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2005, 19:19:05 ; Search time 30 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-818-943-2
Perfect score: 1848
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1848	100.0	345	4	US-09-564-595D-35
3	1848	100.0	345	4	US-09-706-968-43
4	1848	100.0	345	4	US-09-823-033-4
5	1848	100.0	345	4	US-10-139-583-43
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7	1667	90.2	345	4	US-09-457-066-2
8	1667	90.2	345	4	US-09-265-686-2
9	1667	90.2	345	4	US-09-540-224-5
10	1667	90.2	345	4	US-09-564-595D-33
11	1667	90.2	345	4	US-09-706-968-2
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13	1667	90.2	345	4	US-09-823-033-2
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23	1578	85.4	323	4	US-09-468-647A-1
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42	746.5	40.4	370	4	US-10-039-847A-4	Sequence 4, Appl
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45	713	38.6	168	4	US-09-468-647A-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-09-457-066-43
; Sequence 43, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hait, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-457-066-43

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RESULT 2
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; Sequence 35, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
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; ORGANISM: Mus musculus
US-09-564-595D-35

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RESULT 4
US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
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; SEQ ID NO 4
; LENGTH: 345
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; ORGANISM: Mus musculus
US-09-823-033-4

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RESULT 3
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; Sequence 43, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
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RESULT 5

US-10-139-583-43

; Sequence 43, Application US/10139583

; Patent No. 6814965

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/10/139,583

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 09/457,066

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 43

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-139-583-43

Query Match 100.0%; Score 1848; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHTYPRNMLVRLVAVDENVRILTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMLVRLVAVDENVRILTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GWCGSGTVPKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GWCGSGTVPKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYKKSQVNLNL 240
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYKKSQVNLNL 240
Qy 241 LKEEVLKXSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLKXSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQRLPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

RESULT 6

US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 4; Length 345;

; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 3; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHTYPRNMLVRLVAVDENVRILTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PRFPHTYPRNMLVRLVAVDENVRILTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCGSGTVPKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYKKSQVNLNL 240
Db 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWQLLGAFLYKKSQVNLNL 240
Qy 241 LKEEVLKXSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVLKXSCTPRNFSVSIREBLKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQRLPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

RESULT 7

US-09-457-066-2

; Sequence 2, Application US/09457066

; Patent No. 6432673

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-457-066-2

Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSSA 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLKAFYKSKSVVNLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 8
US-09-265-686-2
Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Patent No. 6455283
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
FILE REFERENCE: P1122P2
CURRENT APPLICATION NUMBER: US/09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-265-686-2

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSSA 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLKAFYKSKSVVNLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 9
US-09-540-224-5
Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Patent No. 6468543
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-540-224-5

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRVVTISNGSIHS 60
DB 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60

QY 61 PKFPHYPRNMVLRVAVDENVRVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGSVL 120
DB 61 PRFPHYPRNTVLVRLVAEENVMVQLTDFDRFGLGLEDPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSSA 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLKAFYKSKSVVNLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLKAFVFGKRSRVVDLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 10
US-09-564-595D-33
Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10

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; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-33

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISGNGSIHS 60
DB 1 MSLFGLLLTTSALAGORCTQAESNLSSKQFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PKPHTYPRNNMVLVRLVAVDENVRIQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGVL 120
DB 61 PRPHTYPRNTVLVRLVAVDENVWIQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGITL 120
QY 121 GRWCSGTVPKGKOTSGKNHRIIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPVLPSSA 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKRSRVVDNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGRLHSLTDVALEHHEECDCVCRGSTGG 345
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RESULT 12

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US-09-723-749-2
; Sequence 2, Application US/09723749
; Patent No. 6620784
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2D1
; CURRENT APPLICATION NUMBER: US/09/723,749
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-723-749-2

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISGNGSIHS 60
DB 1 MSLFGLLLTTSALAGORCTQAESNLSSKQFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PKPHTYPRNNMVLVRLVAVDENVRIQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGVL 120
DB 61 PRPHTYPRNTVLVRLVAVDENVWIQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGITL 120
QY 121 GRWCSGTVPKGKOTSGKNHRIIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSGTVPKGQISKGNIQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTTEAVSPVLPSSA 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRFTWQLLGKAFVFGKRSRVVDNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGRLHSLTDVALEHHEECDCVCRGSTGG 345
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RESULT 11

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US-09-706-968-2
; Sequence 2, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-2

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHERVVTISGNGSIHS 60
DB 1 MSLFGLLLTTSALAGORCTQAESNLSSKQFQSSNKQNGVQDPQHERIITVSTNGSIHS 60
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RESULT 13
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
Db 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PKPHTYPRNMVLVWRLVAVDENVRILQTLTDFRFGLEDPEDDICKYDFVEEPEPSDGV 120
Db 61 PRFHTYPRNTVLVWRLVAVDENVRILQTLTDFRFGLEDPEDDICKYDFVEEPEPSDGV 120

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTETTSPLPSS 180
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTETTSPLPSS 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240

QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300

QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRGNAGG 345

RESULT 15
US-09-468-647A-110
; Sequence 110, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-110

Query Match          90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 7.4e-175;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60
Db 1 MSLFGLLLTTSALAGQRTGTRAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PKPHTYPRNMVLVWRLVAVDENVRILQTLTDFRFGLEDPEDDICKYDFVEEPEPSDGV 120
Db 61 PRFHTYPRNTVLVWRLVAVDENVRILQTLTDFRFGLEDPEDDICKYDFVEEPEPSDGV 120

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTETTSPLPSS 180
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTETTSPLPSS 180

QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240

QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300

QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRGNAGG 345

RESULT 14
US-09-468-647A-101
; Sequence 101, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
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Qy	61	PKFPHTYPRNNVVLVWRLVAVDENVRIQLTFDRFGLGEDPEDDI	CKYDFVEVEEPEPDSGVL	120
Db	61	PRFPHTYPRNTVLVWRLVAVDENVWIQLTFDRFGLGEDPEDDI	CKYDFVEVEEPEPDSGTL	120
Qy	121	GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYISIMPQVTETTS	SPSVLPSPSS	180
Db	121	GRWCGSGTVPGKQISKGNQIRIRFVSDYFPEPFGFCHYINVMQFTEAVS	SPSVLPSPSA	180
Qy	181	LSLDLNNNAVTAFTSLEBLIRYLEPDRQVOLDLSIKPTWQLLGKAFY	GKKSQVNNL	240
Db	181	LPDLNNNAITAFSTLEDLIRYLEPERQOLDLEDYRPTWQLLGKAFY	GKRKSRVVDNL	240
Qy	241	LKEEVKLYSCTPRNFSVSIIBELKRTDTIIFWPGCLLVKRCGNCACCLH	NCNCCQVPRK	300
Db	241	LTEEVRLYSCYPRNFSVSIIBELKRTDTIIFWPGCLLVKRCGNCACCLH	NCNCCQVPSK	300
Qy	301	VTKKYHEVLQRPKTVGKGLHKLSLTDVALEHHEHCDCVCRGNAGG	345	
Db	301	VTKKYHEVLQRPKTVGRLGHKLSLTDVALEHHEHCDCVCRGSTGG	345	

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OM protein - protein search, using sw model

Run on: September 3, 2005, 19:21:57 ; Search time 109.5 Seconds
(without alignments)
1240.813 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHEDCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCT05_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1848	100.0	345	9	US-09-823-033-4
2	1848	100.0	345	9	US-09-818-943-2
3	1848	100.0	345	9	US-09-852-209A-7
4	1848	100.0	345	11	US-09-876-813-35
5	1848	100.0	345	13	US-10-139-583-43
6	1848	100.0	345	14	US-10-131-600-7
7	1848	100.0	345	14	US-10-264-361-4
8	1848	100.0	345	15	US-10-303-997B-7
9	1848	100.0	345	15	US-10-664-432-4
10	1848	100.0	345	15	US-10-439-337A-7
11	1848	100.0	345	16	US-10-664-432-4

12	1848	100.0	345	16	US-10-877-623-35	Sequence 35, Appl
13	1848	100.0	345	17	US-10-938-375-4	Sequence 4, Appli
14	1848	100.0	345	20	US-11-021-088-43	Sequence 43, Appl
15	1848	100.0	345	20	US-11-080-803-35	Sequence 35, Appl
16	1667	90.2	345	9	US-09-823-033-2	Sequence 2, Appli
17	1667	90.2	345	9	US-09-923-935-4	Sequence 4, Appli
18	1667	90.2	345	9	US-09-795-006A-149	Sequence 149, App
19	1667	90.2	345	9	US-09-978-295A-488	Sequence 488, App
20	1667	90.2	345	9	US-09-978-697-488	Sequence 488, App
21	1667	90.2	345	9	US-09-978-192A-488	Sequence 488, App
22	1667	90.2	345	9	US-09-999-832A-488	Sequence 488, App
23	1667	90.2	345	10	US-09-978-189-488	Sequence 488, App
24	1667	90.2	345	10	US-09-796-753-6	Sequence 6, Appli
25	1667	90.2	345	10	US-09-978-608A-488	Sequence 488, App
26	1667	90.2	345	10	US-09-978-585A-488	Sequence 488, App
27	1667	90.2	345	10	US-09-978-191A-488	Sequence 488, App
28	1667	90.2	345	10	US-09-978-403A-488	Sequence 488, App
29	1667	90.2	345	10	US-09-978-564A-488	Sequence 488, App
30	1667	90.2	345	10	US-09-999-833A-488	Sequence 488, App
31	1667	90.2	345	10	US-09-981-915A-488	Sequence 488, App
32	1667	90.2	345	10	US-09-978-824-488	Sequence 488, App
33	1667	90.2	345	10	US-09-918-585A-488	Sequence 488, App
34	1667	90.2	345	10	US-09-999-834A-488	Sequence 488, App
35	1667	90.2	345	10	US-09-978-423A-488	Sequence 488, App
36	1667	90.2	345	10	US-09-978-193A-488	Sequence 488, App
37	1667	90.2	345	10	US-09-999-830A-488	Sequence 488, App
38	1667	90.2	345	10	US-09-978-757A-488	Sequence 488, App
39	1667	90.2	345	10	US-09-978-187B-488	Sequence 488, App
40	1667	90.2	345	10	US-09-978-643A-488	Sequence 488, App
41	1667	90.2	345	10	US-09-978-375A-488	Sequence 488, App
42	1667	90.2	345	10	US-09-978-298A-488	Sequence 488, App
43	1667	90.2	345	10	US-09-978-188A-488	Sequence 488, App
44	1667	90.2	345	10	US-09-978-681A-488	Sequence 488, App
45	1667	90.2	345	10	US-09-978-194A-488	Sequence 488, App

ALIGNMENTS

RESULT 1
US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823.033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-823-033-4

Query Match	100.0%;	Score	1848;	DB	9;	Length	345;
Best Local Similarity	100.0%;	Pred. No.	1.2e-166;				
Matches	345;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MLLGLLLLTALAGQRTGTAEENLSSKQLSSDKQNGVQDPRHVRVTTISNGSGVHS	60				
Db	1	MLLGLLLLTALAGQRTGTAEENLSSKQLSSDKQNGVQDPRHVRVTTISNGSGVHS	60				
Qy	61	PKFPHYPRNVLVRLVAVDENVRILQTFDERGLEDDPEDDICKYDFVEEPEPSDGSVL	120				
Db	61	PKFPHYPRNVLVRLVAVDENVRILQTFDERGLEDDPEDDICKYDFVEEPEPSDGSVL	120				
Qy	121	GRWCGSTVPGKQTSKGNHRIRVSDYPPSPGFCIHYSIIIMPQVTTTSPSVLPDPS	180				
Db	121	GRWCGSTVPGKQTSKGNHRIRVSDYPPSPGFCIHYSIIIMPQVTTTSPSVLPDPS	180				

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Db 121 GRWCGSTVPKGQTSKGNHIRIRFVSDYFSPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 2
US-09-818-943-2
; Sequence 2, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHYPRNMVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCGSTVPKGQTSKGNHIRIRFVSDYFSPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSTVPKGQTSKGNHIRIRFVSDYFSPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 3
US-09-852-209A-7
; Sequence 7, Application US/09852209A
; Patent No. US20020164687A1
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; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDPRHVRVTTISNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDPRHVRVTTISNGSIHS 60
Qy 61 PKFPHYPRNMVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCGSTVPKGQTSKGNHIRIRFVSDYFSPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSTVPKGQTSKGNHIRIRFVSDYFSPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPRDQVLDLSLYKPTWQLLGAFLYKSKSKVNNLN 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 4
US-09-876-813-35
; Sequence 35, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
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; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-813-35

Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 PKFPHYPRNMVWRLVAVDENVRVQLTDFERFGLDEPDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTSLLEELIRYLEPDRWQVLDLSYKPTWLLGKAFLYGKSKVNNLNL 240
DB 181 LSLDLLNNAVTAFTSLLEELIRYLEPDRWQVLDLSYKPTWLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5

US-10-139-583-43
; Sequence 43, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-583-43

Query Match 100.0%; Score 1848; DB 13; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVWRLVAVDENVRVQLTDFERFGLDEPDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRVQLTDFERFGLDEPDDICKYDFVEVEEPPSDGSVL 120
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DB 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
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DB 181 LSLDLLNNAVTAFTSLLEELIRYLEPDRWQVLDLSYKPTWLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345

RESULT 6

US-10-131-600-7
; Sequence 7, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOUTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-131-600-7

Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60

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Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDP RHERVVTISGNGSIHS 60
QY 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
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RESULT 7

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US-10-264-361-4
; Sequence 4, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-264-361-4
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Query Match 100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDP RHERVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDP RHERVVTISGNGSIHS 60
QY 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
```

RESULT 8

```
US-10-303-997B-7
; Sequence 7, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-303-997B-7
```

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Query Match 100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDP RHERVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKEQNGVQDP RHERVVTISGNGSIHS 60
QY 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKPPTYPRNMVLVWRLVAVDENVR IQLTFDRFGLGLED PEDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGKTSKGNHIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
```

RESULT 9

```
US-10-664-432-4
; Sequence 4, Application US/10664432
; Publication No. US20040043031A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
```

```
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-432-4

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 10
US-10-439-337A-7
; Sequence 7, Application US/10439337A
; Publication No. US20040053837A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND
; FILE REFERENCE: 029065.44740C4
; CURRENT APPLICATION NUMBER: US/10/439,337A
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/303,997
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 345
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; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-439-337A-7

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 11
US-10-664-432-4
; Sequence 4, Application US/10664432
; Publication No. US20040228870A9
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-432-4

Query Match      100.0%; Score 1848; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKEQNGVQDPRHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHTYPRNMVWRLVAVDENVRILQITFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNLNL 240
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QY 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345

RESULT 12

US-10-877-623-35
; Sequence 35, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-877-623-35

Query Match 100.0%; Score 1848; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITSAAGORTGTRAESNLSSKQLQSSDKEQGVQDPRHVRVTTISNGSIHS 60
Db |||||
1 MLLGLLLITSAAGORTGTRAESNLSSKQLQSSDKEQGVQDPRHVRVTTISNGSIHS 60
QY 61 PKFPHTYPRNMVWLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db |||||
61 PKFPHTYPRNMVWLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db |||||
121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLL 240
Db |||||
181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLL 240
QY 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345

RESULT 13

US-10-938-375-4
; Sequence 4, Application US/10938375
; Publication No. US20050049218A1
; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/938,375
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-938-375-4

Query Match 100.0%; Score 1848; DB 17; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITSAAGORTGTRAESNLSSKQLQSSDKEQGVQDPRHVRVTTISNGSIHS 60
Db |||||
1 MLLGLLLITSAAGORTGTRAESNLSSKQLQSSDKEQGVQDPRHVRVTTISNGSIHS 60
QY 61 PKFPHTYPRNMVWLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db |||||
61 PKFPHTYPRNMVWLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db |||||
121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLL 240
Db |||||
181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVVNLL 240
QY 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db |||||
241 LKEEVKLYSCTPRNFSVSIRESLKRDTDTIFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345
Db |||||
301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEEDCDVCRCGNAGG 345

RESULT 14

US-11-021-088-43
; Sequence 43, Application US/11021088
; Publication No. US20050159358A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/11/021,088
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-021-088-43

Query Match 100.0%; Score 1848; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 15
US-11-080-803-35
; Sequence 35, Application US/11080803
; Publication No. US20050164937A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/11/080,803
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1993-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-080-803-35

Query Match 100.0%; Score 1848; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240

Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQLRPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

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